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1 GATACATAAATCTTCAACACAACTCTTTAATTATCTAGTTTAATACAAATGGCGGCGATA 60

Query Match 100.0%; Score 1188; Best Local Similarity 100.0%; Pred. No. 0; Matches 1188; Conservative 0; Mismatches

DB 6;

Length 1188; Indels 0;

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FEATURES SOURCE	RESULT 1 E63071 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	19 178 20 179 20 179 20 176 20 169 221 169 224 163 27 161 30 151 144 20 33 114 410 245 56 6 6 45 56 6 6 56 6 6 6 6 6 6 6 6 6
FT Key Location/Qualifiers FT CDS (49)(1020).  11188 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702"	1188 bp DNA linear PAT 27-AUG-2002 DNA encoding chlorophylase and plant transformed by it. E63071 E63071.1 G1:22553554 JP 2001086990-A/2. Arabidopsis thaliana (thale cress) Arabidopsis thaliana (thale cress) Arabidopsis thaliana (thale cress) Arabidopsis thaliana EUMARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  1 (bases 1 to 1188) Tsuchiya, T., Ota, H., Takamiya, K., Harada, S. and Nakat, K. DNA encoding chlorophylase and plant transformed by it RAGOME CO LTD OS Arabidopsis thaliana (thale cress) PN JP 2001086990-A/2 PD 03-APR-2001 PP 20-SEP-1999 JP 199266181 PI TORU TSUCHIYA, HIROYUKI OTA, KENICHIRO TAKAMIYA, SATOSHI HARADA, PI KENGO NAKATA PC C12N15/00, C12N5/10, C12N9/16//(C12N9/16, C12R1:19), PC C12N15/00	8.8 15.1 1444 6 AX411613 AX411613 AX411613 Sequence 14.9 1157 15 AY292526 Ginkgo bi 14.9 114.3 1216 6 AX411603 AX411603 Sequence 25.4 14.3 1104 15 AF337545 AF337546 AF337545 AF337546 AF34760 AF337546 A

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Benedetti,C.E., Costa,C.L., Tu
Direct Submission
Submitted (26-AUG-1997) Centro
Genetica, University of Campin
Location/Qualifiers
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1 (bases 1 to 1188)
Benedetti, C.E., Costa, C.L., Turcinelli, S.R. and Arruda, P.
Differential expression of a novel gene in response to coronatine, methyl jasmonate, and wounding in the Coil mutant of Arabidopsis plant Physiol. 116 (3), 1037-1042 (1998)
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vritcptvactypvvlffhcfylrnvrysdvlnhiashgyilvapqlckllppgoque
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fsaligidpvactnkyirtdphilitykpesfeldipvavvgtglgpkynnvmppcapt
dlnhesfykeckatkahfvaadyghnmhldddlpgfvgfmagcmckngqrkksemrsf
vggivvaflkyslwgekaeirlivkdpsvspakldpspelebasgifv"
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and wounding
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/protein_id="AAC13947.1"
/db_xref="GI:2460203"
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/cultivar="Columbia;
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Query Match Best Local Sim Matches 1175;

Similarity

98.9%;

Score 1175; Pred. No. 0; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinnzaki, K., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Salk, Stanford, PGEC (SSP) Consortium members carried sequencing and annotation of the RAFL cDNAs: Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M. K Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rospids; eurosdas II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e-mail for correspondence: arab@sequence.stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-APR-2002) DNA Sequencing and Technology Stanford University, 855 California Avenue, Palo Alto,
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FSALIGIDPVAGTNKYIRHDPHILTYKPESFELDIPVAVVGTTAGAKWNWAPPCAPT
DLNHEEFYKECKATKAHFVAADYGHWDMLDDDLPGFVGFMAGCWCKNGQRKKSEMRSF
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/protein_id="AAM20666.1"
/db_xref="GI:20466698"
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                                                                                                                                                                                                                                                                                                                                                         /gene="At1g19670"
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/note="This clone in
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/chromosome="1"
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[mol_type="mRNA"]
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                                                                                                                                                                                                                                                                            gene="At1g19670"
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                                                             AGATTTGTGTTATGTACTATTATCAGAGGGGTCTTGAATATTTGAAAAAACCTATCAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA; 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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Submitted (19-SEP-2002) DNA Sequencing and Technology Center,
Submitted University, 855 California Avenue, Palo Alto, CA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contrequally to this work. Shinozaki,K. (RIKEN GSC) and Dav (SSP/Stanford) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pENTR (ORF) clones using the RAFL cDNAs: Nguyen,M., Southwick,A., Tripp,M., Palm(C.J., Jones,T., Wu,T., Chen,H., Cheuk,R., Chan,M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Lee,J.M., Kim,C.J., Quach,H.L., Shinn,P., Tang,C.C., Toroumi,M., Wallender,E.K., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Ecker,J., Theologis,A. and Davis,R.W.
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                      /translation="maaiedsptfssvvtpaafeigslptteipvdpvendstappkp
VRITCETVACTYPVVLFFHCFYLNNYFSDVLNHIASHGYILVAPQLCKLLPPGGQVE
VDDAGSVINMASENLKAHLPTSVNANGKYTSLVHIASHGYILVAPAVALCHAATLDPSI
VDDAGSVINMASENLKAHLPTSVNANGKYTSLVHIASHGYILPAVALCHAATLDPSI
FSALIGIDPVAGTNKYIRTDPHILTYKPESFELDIPVAVVGTGLGPKWNNVMPPCAPT
                                                                                                                                                                                                                                                                                                                                                                                /ecotype="Columbia"
/note="This clone is in
PCR product using RIKEN
a template"
DLNHEEFYKECKATKAHFVAADYGHMDMLDDDLPGFVGFMAGCMCKNGQRKKSEMRSF
                                                                                                                             /product="unknown protein"
/protein_id="AAN15628.1"
/db_xref="GI:23198202"
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/db_xref="taxon:3702"
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                                                           AAGGATCCTTCCGTTTCTCCGGCCAAGCTTGATCCTTCACCTGAGTTGGAAGAAGCTTCT
                                                                                                  TACGGACATATGGATATGTTGGACGATGATTTGCCCCGGTTTTGTTGGGTTTTATGGCCGGT 828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGCGGCGATAGAGGACAGTCCAACGTTTTCCTCTGTGGTAACTCCGGCGGCTTTTGAG
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                                            AAGGATCCTTCCGGTTTCTCCGGCCAAGCTTGATCCTTCACCTGAGTTGGAAGAAGCTTCT
                                                                                                                                                                                  TGTATGTGTAAGAATGGGCAAAGAAAAAAGTCTGAGATGAGGAGCTTTGTAGGTGGAATT
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                                                                                                                                                                                                             TACGGACATATGGATATGTTGGACGATGATTTGCCCCGGTTTTGTTGGGTTTATGGCCGGT
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                                                                                                                                                                                                                                             Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ArG). A sequence is considered to be 3'-truncated if it lacks the creation and sequence that these cDNA sequence is considered to be 3'-truncated if it lacks the Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the full-length clones. Ceres, Inc. carried out the clustering of the figure of the sequences, selection of clones, and sequence assembly.
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Brover, V., Troukhan, M.,
Feldmann, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Brover, V., Troukhan, M.,
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Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-MAR-2002) Ceres,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                 /organism="Arabidopsis
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="31589"
                                                                                                                                                                                                                                     Location/Qualifiers
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                     93.9%;
; Score 1115.4; pred. No. 5.8e-0; Mismatches
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ATACATAAATCTTCAACACAACTCTTTAATTATCTAGTTTTAATACAAATGGCGGCGATAG

ATACATAAATCTTCAACAACTCTTTAATTATCTAGTTTAATACAAATGGCGGCGATAG

COMMENT On Mar 9, 2000 this sequence version replaced gi:7121532.  Bases 1-59,676 of IGF clone F14P1 overlap with IGF clone F6F9, gb Ac007797.  e-mail for correspondence: arab@sequence.stanford.edu Genes with similarity to proteins in the databases are named 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described	1020 AGATTTGTGTTATGTACTATTATCAGAGGGGTCTTGGATATTTTGAAAACCTATCAATGT 1079  1082 TTTCTAGCTCCAAGCTAGCTATTGTTCATGTCCTAAGTTGCATGTGTATTATTATAAAC 1141  1080 TTTCTAGCTCCAAGCTATGTTCATGTCCTAAGTTGCATGTGTATTTTTATTAAAC 1139  1142 TCGATCAAAACATTTGT 1158
REFERENCE 5 (bases 1 to 90341) AUTHORS Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologis, A. and Davis, R.W.  TITLE Direct Submission JOURNAL Submitted (12-SEP-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,	900 TCAAGTATAGTTTTGTGGGGTGAAAAAGCGGAGATTCGATTGATT
AUTHORS Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologis and Davis, R.W.  TITLE Direct Submission JOURNAL Stanford University, 855 California Avenue, Palo Alto, CA 94304 USA	ATGGGCAAAGAAAAAGTCTGAGATGAGAGCTTTGTAGGTGGAATTGTGGTTGCGTTTC
Thaveri, Theologi Direct S Submitte Stanford USA	722 TTTACAAAGAGTGTAAGGCGAACGAAAGCCCATTTCGTGGCTGCCGATTACGGACATATGG 781
USA  3 (bases 1 to 90341)  REFERENCE 3 (bases 1 to 90341)  AUTHORS Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, J. Altafi, H., Nguyen, M., Lam, B., Southwick, A., Bei, Q., Buehll Chin, C., Chiou, J., Choi, E., Dunn, P., Gonzalez, A., Howng, B. Koo, T., Lee, J. M., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., MNLharsky, N., Pham, P., Sakano, H., Schwartz, J., Shinn, P., MNLharsky, N., Pham, P., Sakano, H., Schwartz, J., Shinn, P.,	
Altafi, H., Nguyen, M., Lam, B., Southwick, A., Bei, Q., Buehler, E., Chin, C., Chiou, J., Choi, E., Dunn, P., Gonzalez, A., Howng, B., Kim, Koo, T., Lee, J.M., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukhareky, N., Pham, P., Sakano, H., Schwartz, J., Shimn, P., Thaveri, A., Toriumi, M., Vaysberg, M., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.  TITLE Direct Submission  JOURNAL Submitted (01-MAR-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,	482 TIGGGTIGGGCTAGGCCATGCACATTAGACCCATCAGCTTTTCAGCTCTAA 541
Altafi,H., Nguyen,M., Lam,B., Southwick,A., Miranda,M., Broo Buehler,E., Chao,Q., Chin,C., Chiou,J., Choi,E., Gonzalez,A. Howng,B., Johnson-Hopson,C., Khan,S., Kim,C., Koo,T., Lee,J.; Liu,A., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Shinn,P., Toriumi,M., Vaysberg,M., Yu,G., Ecker,J., Theologi JOURNAL und Davis,R. W. and Davis,R. W. ungublished 2 (bases 1 to 90341)  AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F	ATGCTGGAAGTGTGATAAACTGGGCATCGGAAAACCTCAAAGCTCACCTACCAACTTCGG
ORGANISM Arabidopsis thaliana (thale cress)  ORGANISM Arabidopsis thaliana  Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons  rosids; eurosids II, Brassicales; Brassicaceae; Arabidopsis.  REFERENCE 1 (bases 1 to 90341)  AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,	242 TITATCTTCGCAACTACTTCTACTCTGACGTTCTTAACCACATCGCTTCGCATGGTTACA 301
z Q	122 CGACAACCGAGATACCGGTGGATCCGGTGGAAAATGATTCAACAGCACCGCCAAAACCGG 181
	62 AGGACAGTCCAACGTTTTCCTCTGTGGTAACTCCGGCGGCTTTTGAGATAGGCAGCCTCC 121

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KIGSVRHIMSWLTAFFISFFTLLASLALPQTKEHSQLHSSSVABELCDERIARESRPP
CDDBGTTFMITICATITECT FROM THE COLORY OF THE COLORY OF
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/gene="F14P1.2"

Join (63540. .63596,63685. .63951,64046. .64123,64205. .64306,

64387. .64436,64527. .64626,64741. .64833,64927. .65040,

65139. .65253,65359. .65756)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70742. . 73284
/gene="F14f1.3"
join(70742. .70816,70957. .71382,72084. .72173,72904. .73284)
/gene="F14f1.3"
/note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPPRSTITERVIISSVLSRLGDLEKQIENLHSRKSEMPHEKEELLNAAVYRVDALEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F14P1.1"

join(60210. .60507,60608. .60778,60878. .60927,61025. .61081,

61184. .61249,61387. .61461,61599. .61717,61807. .61960)

/gene="F14P1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/proteIn_id="AAF98406.1"
/db_xref="GI:9795588"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDRPNGQPCFDTKEFDLVRNMMQAVDEERYDEAGKLSLSHPPYLVVILVLINY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="overlap with IGF clone F6F9, gb|AC007797, GenBank record for BAC clone F6F9 for annotation
/gene="F14P1.4"
/note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LITIKKV"
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'chromosome="I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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Best Local Similarity
Matches 1175; Conserv
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                                                 57540
                                                                                                                                              62
                                                 AGGACAGTCCAACGTTTTCCTCTGTGGTAACTCCGGCGGCTTTTGAGATAGGCAGCCTCC
                                                                                                                                         AGGACAGTCCAACGTTTTCCTCTGTGGTAACTCCGGCGGCTTTTGAGATAGGCAGCCTCC 121
                                                                                                                                                                                                                                           ATACATAAATCTTCAACACACTCTTTAATTATCTAGTTTAATACAAATGGCGGCGATAG
                                                                                                                                                                                                                                                                                                 ATACATAAATCTTCAACACAACTCTTTAATTATCTAGTTTAATACAAATGGCGGCGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MVAEALPKCPEAPLVLGLQPAALIDNVAPVDWSLLDQIPGDRGG
SIAVQKDELEHMLKELDAHISVAPLKKVAGGSVTUTVRGLSVGFVATGIIGAYGDDE
QGQLFVSNWGFSGVSISRLRKKKGSTAQCVCLVDDSGRTWAPCLSSAVKIQADELSK
EDFTGSKWLVLRYAVLNLQVIQAAIRFAKQEGLSVSLDLASFEWVRNSKSELRQLLES
GNIDLCFANEDEAAELLRGEQEAGPEAALEFLGRHCRWAVVILGSKGCIAKHDKEVVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(81552...81800,81920...82031,82136
82329...82436,82543...82581,82670...82741,82820.
83225...83365))
/gene="F14P1.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAF98401.1"
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/fdb_xref="G1:9795583"
/fdb_xref="G1:9795683"
/fdb_xref="G1:9795687"

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/db_xref="G1:9795582"
/db_xref="G1:9795582"
/translat.ton="MPEDPRKKSTAGVPPGSDGFPVIGETLQFMLSVNSGKGFYEFVRS
RRIRYGSCFRTSLFGETHVFLSTTESARLVLNNDSGMFTKRYIKSIGELVGDRSLLCA
PQHHHKILRSRLINLFSKRSTALMVRHFDELVVDALGGWEHRGTVVLLTDLLQTFKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(85358. .85648,86056. .86207,86310. .86435,
87001. .87144,87399. .87513)}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISAIGETVATDATGAGDLFASGFLYGLIKGLSLEECCKVGSCSGGSVIRALGGEVTPE
NWQWMHKQLQLKGLPVPDIHN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80606. .80776
/gene="F14P1.6"
80606. .80776
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complement (77375. .78430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="F14P1.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (85358. .87513)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Unknown protein"
/codon start=1
/protein_id="AAF98405.1"
/db_xref="GI:9795587"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FPGFACFCYFNC"
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/protein_id="AAF98402.1"
/db_xref="GI:9795584"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Similar to defensin; Similar to defensin AMP1 (anti
microbial protein)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGRHRHRHGHRSRKHRQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVSQLQNSDVPQWQNGGVLQLQNGDVPQWQTGGVSQLQNGVHEPQNGIVQWKGSRDDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPRLVLQDCEMEGLL"

complement (77375. .78430)
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RERRNEINSHNNHHEDFLQQLLAVDNDTPQLTDAEIKDNILTMIIAGQDTTASALTWM
VKYLGENQKVLDILIEEQSQITKKASNKPFLELEDLSEMPYASKMVKESLRMASVVPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="Unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Unknown protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="F14P1.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="F14P1.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                            o,
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1012; DB 15;
Pred. No. 8.6e-274;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 153; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 90341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .82031,82136. .82233,
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57599

61 57539

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		1049 GGGGTCTTGAATATTTGAAAAACCTATCAATGTTTTCTAGCTCCAAGCTAGCT	
	FEATURES source	989 CTGAGTTGGAAGAAGCTTCTGGTATCTTCGTCTAGATTTGTGTTATGTACTATTATCAGA 1048	
On May Bases ( Bases ( of IGF	COMMENT	929 CGGAGATTCGATTGATGTGAAGGATCCTTCCGTTTCTCCGGCCAAGCTTGATCCTTCAC 988	
Direct Submit Stanfo	TITLE JOURNAL	869 GGAGCTTTGTAGGTGGAATTGTGGTTTGCGTTTCTCAAGTATAGTTTGTGGGGTGAAAAAG 928 	
4 (bar Feders) Altafi	REFERENCE AUTHORS	809 TTGTTGGGTTTATGGCCGGTTGTATGTGTAAGAATGGGCAAAGAAAAAGTCTGAGATGA 868 	
Direct Submit Stanfo	TITLE JOURNAL	749 CCGATTTCGTGGCTGCGGATTACGGACATATGGATATGTTGGACGATGATTTGCCCGGTT 808	
Koo, T. Mukhari Thaver		689 CATGCGCACCAACGGACTTAAACCATGAGGAGTTTTACAAAGAGTGTAAGGCGACGAAAG 748	
3 (bai 3 (bai Federsi Altafi	REFERENCE AUTHORS	629 ACATACCGGTTGCAGTGGTAGGAACCGGACTCGGACCGAAGTGGAACACGTGATGCCAC 688	
Direct Submit Stanfo	TITLE JOURNAL	569 ACAAATACATTAGAACCGATCCGCATATCTTAACGTATAAACCGGAATCTTTCGAGCTGG 628 	
Altafi Altafi Gonzal Luros,	AULIONO	509 CATTAGACCCATCCATCACGTTTTCAGCTCTAATAGGAATTGATCCAGTCGCAGGAACTA 568 	•
and Day	JOURNAL REFERENCE	449 TCGTGGGCCACAGCCGCGGTGGGAAAACGGCGTTTGCGGTTGCGGTAGGCCATGCCGCAA 508	•
Buehle: Howng, I		389 CGGAAAACCTCAAAGCTCACCTACCAACTTCGGTAAATGCTAATGGAAAATACACCTCAC 448 	• •
rosids 1 (ba 1 Feders Feders	REFERENCE AUTHORS	329 TATTGCCGCCGGGAGGGCAAGTGGAAGTGGACGATGCTGGAAGTGTGATAAACTGGGCAT 388	• •
Arabid Arabid Eukary	MS	315ACAGTTGTGCAAAAT 328 57900 TGATTGTTACGTGAAAAGATATAAGTTAATATTTTATATTCTTGAATGACAGTTGTGCAAAAT 57959	•
ACCOUTT ACCOUTT HTG.	ACCESSION VERSION KEYWORDS	57840 AAGGATAACTTACGGTATGTAACATGTAACATGTAAAACAAAATGTACATTAATTGAGAT 57899	•
AC0077 Arabid	4	5780 TTCTTGTAGCCCCACAGGTACATAATTTAACTATACAAAAAATAATTATGAATCATTTAA 57839 315	
		TTTATCTTCGCAACTACTTCTACTCTGACGTTCTTAACCACATCGCTTCGCATGGTTACA	. • .
ATGT	Db 58740	182 TGAGAATCACCTGTCCAACAGTCGCCGGAACTTATCCCGTCGTTTTATTCTTCCATGGCT 241	• ,
	t D	122 CGACAACCGAGATACCGGTGGATCCGGTGGAAAATGATTCAACAGCACCGCCAAAACCGG 181 	• ,

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밁 ð В 5 밁 ð 밁 δ 밁 ð 밁 S 밁 Ś 밁 8 밁 δ 밁 S 밁 S 밁 S 밁 Ş

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ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; macophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; bases I to 11942)
bases I to 119942)
rspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., rspiel, N.A., Chin, C.J., Southwick, A., Miranda, M., Brooks, S., fi, H., Nguyen, M., Lam, B., Southwick, A., Miranda, M., Brooks, S., ler, B., Chao, Q., Chin, C., Chiou, J., Choi, E., Gonzalez, A., ler, B., Chao, C., Khan, S., Kim, C., Koo, T., Lee, J.M., C., Liu, A., Liu, S., Mukharsky, N., Pham, P., Sakano, H., Ch., P., Toriumi, M., Vaysberg, M., Yu, G., Ecker, J., Theologis, A., Navis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                   Dases 1 to 119942)
rspiel,N.A., Palm,C.J., C.
i,H., Nguyen,M., Lam,B.,
avis,R.W.
                                                                                                                         y 16, 2000 this sequence version replaced gi:7547094.
s 60,267-119,942 of BAC clone F6F9 overlap with bases 1-59,676
sr clone F14P1, AC024609 and bases 1-3,490 of BAC clone F6F9
lap with bases 89,221-92,710 of BAC clone T20H2, AC022472.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 t Submission
|tted (16-MAY-2000) DNA Sequencing and Technology Center,
|Cord University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pages 1 to 119942)

reple1, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Fighte1, N.A., Palm, C.J., Rowley, D., Buehler, E., Dunn, P., Il, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Ilez, A., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Ilez, A., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., J.S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., J., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., J., Tu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                          t Submission
Lted (12-SEP-2000) DNA Sequencing and Technology Center,
Lted (12-SEP-2000) ENA Sequencing and Technology Center,
Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "spiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., I., H., Nguyen, M., Lam, B., Southwick, A., Bei, Q., Buehler, E., C., Chiou, J., Choi, E., Dunn, P., Gonzalez, A., Howng, B., Kim, J., Lee, J.M., Lenz, C., Li, J., Liu, J., Liu, K., Liu, S., Yrsky, N., Pham, P., Sakano, H., Schwartz, J., Shinn, P., ri, A., Toriumi, M., Vaysberg, M., Walker, M., Yu, G., Ecker, J., ogis, A., and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                t Submission
Lted (12-UN-1999) DNA Sequencing and Technology Center,
Cted University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ases 1 to 119942)
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Liu, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSRAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (join (8394. .8526, 8930. .9215, 9321. .9399))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (8394. .9399)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'clone="F6F9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAGMAIGIVGDAGVRANAQQPKLFVGMILILIFAEALALYGLIVGIILSSRAG
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Query Match
Best Local Similarity
Matches 1175; Conserv
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                                                                                                                                                                         YRYNLQPGGGPNPEMVNSSNNNQRPRDSKPKIMKACMYFNSARGCRHGANCMYQHDAT
PYQPRNLNNGNINTSDMQNAKRMRFDRD"
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pgtvalretrkyqkstdllirklpfqrlyretaqdfkydlrfqshavlalqeaaeayl
yglfedtnlcathakrytimskolqlarrirgera"
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/protein_id="AAG12563.1"
/db_xref="GI:10086503"
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                                85.2%;
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                                       Pred. No.
                                                                        Score 1012;
   Mismatches
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   8.6e-274;
ches 0;
                                                                        DB 15;
   Indels 153; Gaps
                                                                 Length 119942;
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241	118766 GGAGCTTTGTAGGTGGAATTGTGGGTTGCGTTTCTCAAGTATAGTTTGTGGGGTGAAAAAG 928
	TIGTTGGGTTTATIGGCCGGTTGTATGTGTAAGAATGGGCAAAGAAAAAGTCTGAGATGA
121 229	
169	689 CATGCGCACCAACGGACTTAAACCATGAGGAGTTTTACAAAGAGTGTAAGGCGACGAAAG 748 
109	629 ACATACCGGTTGCAGTGGGAACCGGACTCGGACCGAAGTGGAACAACGTGATGCCAC 688 
Best Local Similarit Best Local Similarit Conscipence Matches 975; Consc	569 ACAAATACATTAGAACCGATCCGCATATCTTAACGTATAAACCGGAATCTTTCGAGCTGG 628 
ORIGIN	509 CATTAGACCCATCCATCACGTTITCAGCTCTAATAGGAATTGATCCAGTCGCAGGAACTA 568 
	449 TCGTGGGCCACAGCCGCGGTGGGAAAACGGCGTTTGCGGTTGCGCTAGGCCATGCCGCAA 508
JOURNAL PATEUT. WE SYNGENTE HIL CHAPEL HIL Jeffrey L.	389 CGGAAAACCTCAAAGCTCACCTACCAACTTCGGTAAATGCTAATGGAAAATACACCTCAC 448 
REFERENCE 1  REFERENCE 1  AUTHORS Glazebrook  TITLE plant gene infection	329 TATTGCCGCCGGGAGGGCAAGTGGAAGTGGACGATGCTGGAAGTGTGATAAACTGGGCAT 388 
ORGANISM Arabidopsi Eukaryota; Spermatods; eu	315
	118106 AAGGATAACTTACGGTATGTAACATGTAACATGTAAAACAAAATGTACATTAATTGAGAT 118165
DEFINITION Sequence 3 ACCESSION AX412268	315
RESULT 8 AX412268 AX412268 AX412268	302 TTCTTGTAGCCCC314
	242 ITTATCTTCGCAACTACTTCTACTCTGACGTTCTTAACCACATCGCTTCGCATGGTTACA 301 
119006	117926 TGAGAATCACCTGTCCAACAGTCGCCGGAACTTATCCCGTCGTTTTATTCTTCCATGGCT 117985
1109	CGACAACCGAGATACCGGTGGATCCGGTGGAAAATGATTCAACAGCACCGCCAAAACCGG
Qy 1049 GGGGTCTT	CGACAACCGAGATACCGGTGGATCCGGTGGAAAATGATTCAACAGCACCGCCAAAACCGG
Db 118886 CTGAGTTG	62 AGGACAGTCCAACGTTTTCCTCTGTGGTAACTCCGGCGGCTTTTGAGATAGGCAGCCTCC 121
118826	2 ATACATAAATCTTCAACACAACTCTTTAATTATCTAGTTTAATACAAATGGCGGCGATAG 61 

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Participations AG (CH); UNIVERSITY OF NORTH CAROLINA AT ILL (US); Glazebrook, Jan (US); Wang, Xun (US); Dangl, L. (US); Eulgem, Thomas (US)

Location/Qualifiers

    a; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
phyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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                                                                               SGTTACATTCTTGTAGCCCCCACAGTTGTGCAAATTATTGCCGCCGGGAGGGCAA 348
                                                                                                                                                        ATGGCTTTTATCTTCGCAACTACTTCTACTCTGACGTTCTTAACCACATCGCT
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/mol_type="unassigned DNA"
/db_xref="taxon:3702"
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RESULT 9
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Sequence 233 1
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                                               Glazebrook, J., Wang, X., Dangl, J.L., Eulgem, T. and Zhu, T.
Plant genes, the expression of which are altered by path
infection
Patent: WO 0222675-A 233 21-MAR-2002;
Syngenta Participations AG (CH); UNIVERSITY OF NORTH CA:
CHAPEL HILL (US); Glazebrook, Jan (US); Wang, Xun (US)
Jeffrey L. (US); Eulgem, Thomas (US)
Location/Qualifiers
                                                                                                                                              Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/mol_type="unassigned [
/db_xref="taxon:3702"
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Taipei, Taiwan 11529, Republic of
Location/Qualifiers
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Chen, H.-H., Chou, Y.-F. and
Direct Submission
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/note="BoCLH1"
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1 (bases 1 to 1115)
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/protein_id="ANNS1933.1"
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VDDAGKVINGTSKNIKAHLPSSVNANGNYTALVGHSRGKTAFAVALGHAATLDPSIE
EVNHEEFYIECKATKGHFVAADYGHMDNLDDNLFGFVGFMAGCKNGKKKSEMRSF
EVNHEEFYIECKATKGHFVAADYGHMDNLDDNLFGFVGFMAGCKNGKKKSEMRSF
                                                                                                                                                                                                                                                                                                                                                                  /organism="Brassica oleracea"
/mol type="mRNA"
/cultivar="Green king"
/db xref="taxon:3712"
/tissue_type="floret"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of Botany,
China
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Query Match
Best Local Similarity
Matches 862; Conserv
                       GCTTCTGGTATCTTCGTCTAGATTTGTGTTATGTACTATTATCAGAGGGGTCTTGAATAT 1062
                                                                                            ATTGTGAAGGATCCTTCCGTTTCTCCGGCCAAGCTTGATCCTTCACCTGAGTTGGAAGAA
                                                                                                                                                GGAATTGTGGTTGCGTTTCTAAAGTATAGTATATGGGGTGAAATGTCAGAGATTCGACAG
                                                                                                                                                                       GGAATTGTGGTTGCGTTTCTCAAGTATAGTTTTGTGGGGTGAAAAAGCGGAGATTCGATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTCACCTCCCAAGTTCAGTAAAACGCTAATGGCAACTACACCGCACTCGTGGGTCATAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTAGCTTCTCATGGCTACATTGTTGTAGCCCCACAGCTTTGCAAGATTTTGCCGCCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTTTATTCTTCCATGGCTTTTATCTTCGCAACTACTTCTACTCTGACGTTCTTAACCAC 282
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GCTTCTGGTTATCTCGTCTAGATTTGTGGTTATGTAACGTATTGGTATCCCCAGAAAGAC
                                                                                                                                                                                                                      GCGGGTTGTATGTGTAAGAACGGTAAACGCAAAAAGAGTGAGATGAGAAGCTTTGTTGGT
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Pred. No. 4.9e-201;
0; Mismatches 180;
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AUTHORS
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VERSION
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ORGANISM
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Matches 400; Conserv
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-MAY-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK

Lane, Norwich, NR4 7UJ, UK

AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a graph dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, MT a defective suppressor mutator transposon. 3 denotes a sequence derived from the 3'end of the transposon BSRC GARNet, ATIS project
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Unpublished
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STS; Sequence tagged site.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rossids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                      TGCGGTTGCGCTAGGCCATGCCGCAACATTAGACCCATCCACGTTTTCAGCTCTAAT
                                                                                                                                                                                                                                                            TGCTGGAAGTGTGATAAACTGGGCATCGGAAAACCTCAAAGCTCACCTACCAACTTCGGT
                                                                                                                                                                                                                                                                                                                                    TCTTGTAGCCCCACAGTTGTGCAAATTATTGCCGGCGGAGGGCAAGTGGAAGTGGACGA
                                        AGGAATTGATCCAGTCGCAGGAACTAACAAATACATTAGAACCGATCCGCATATCTTAAC
                                                                                                                                                                                                    AAATGCTAATGGAAAATACACCTCACTCGTGGGCCACAGCCGCGGGGGAAAACGGCGTT
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                 AGGAATTGATCCAGTCGCAGGAACTAACAAATACATTAGAACCGATCCGCATATCTTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/varTety="Columbia-0 NASC stock

/db_xrefs="taxon:3702"

/clone="ACC24609"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name="SM_3.40564"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Derived from superpool
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transposon
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Pred. No. 5.2e-100;
0; Mismatches 7;
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LeGrys, C.,
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Jones,J.D.
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STS SM_3.40564, sequence
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Patent: WO 0229022-A 1 11-APR-2002;
E.I. DU PONT DE NEMOURS AND COMPANY
Location/Qualifiers
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Sequence 1 from
AX411601
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                                                                                                        ATCCGCATATCTTAACGTATAAACCGGAATCTTTCGAGCTGGACATACCGGTTGCAGTGG
                                                                                                                                                                   CGTTTTCAGCTCTAATAGGAATTGATCCAGTCGCAGGAACTAACAAATACATTAGAACCG
ACTTAAACCATGAGGAGTTTTACAAAGAGTGTAAGGCGACGAAAGCCCATTTCGTGGCTG
                                                         TGGGAACCGGACTCGGACCGAAG----TGGAACAACGTGATGCCACCATGCGCACCAACGG
                                                                                       TTCCCAAAATCCTAACCTATGTTCCTCATTCCTTCAATCTAGCAATCCCAGTTTGCGTAA
                                                                                                                                                 ACTTCTCAGCCCTACTAGGACTAGACCCTGTTGGTGGGTTGAGTAAATGTTGCCAAACAG
                                                                                                                                                                                                          GGGGAAAGACAGCATTTGCTCTGGCACTAGGGTATGC-----TGATACATCCCTCA
                                                                                                                                                                                                                                TGCTCCCAGAAAATGTGAAACCAGACCTACTCAAGCTTGCTCTTTCAGGCCACAGCAGAG
                                                                                                                                                                                                                                                                                                  ACCTACCAACTTCGGTAAATGCTAATGGAAAATACACCTCACTCGTGGGCCACAGCCGCG
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/mol_type="unassigned
/db_xref="taxon:3604"
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Patent WO0229022.
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Pred. No. 6.7e-56;
0; Mismatches 336;
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Best Local Similarity
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Glycine max
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
cosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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E.I. DU
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Sequence 7 from Patent W00229022.
AX411607
AX411607.1 GI:21444162
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                                                                                                                                                                                                                                                                     TATCCCGTCGTTTTATTCTTCCATGGCTTTTATCTTCGCAACTACTTCTACTCTGACGTT
                                                                                                                                                                                                                                                                                                                                  AATGATTCAACAGCACCGCCAAAACCGGTGAGAATCACCTGTCCAACAGTCGCCGGAACT
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              GTTTTATCAGGTCACAGCAAGGGTGGCAAAACTGTATTTGCTGTGGCACTTGGTTATGCT
                                     TCACTCGTGGGCCACAGCCGCGGTGGGAAAACGGCGTTTGCGGTTGCGCTAGGCCATGCC
                                                                                                  GCATCGGAAAACCTCAAAGCTCACCTACCAACTTCGGTAAATGCTAATGGAAAAATACACC
                                                                                                                                 CGGTCTATGTTGGAACCTGGTGATGAAGTTAAATTTGCAGGGAAAGTTGTGGATTGGCTA
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                                                                                                                                                                                            CTAGGCCACATAGCTTCACATGGATTCATAATTGTTGCTCCTCAGCTGTGTTGGAGTGTA
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                                                                       GCCGAGGAGGGGCTTCAACCTCTGCTTCCAGAGAATGTTGAAGCCAAATTGGATAAATTG
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/mol_type="unassigned Dl
/db_xref="taxon:3847"
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                                                                                                                                                             --GGGAGGGCAAGTGGAAGTGGACGATGCTGGAAGTGTGATAAACTGG---
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Pred. No. 1.6e-45;
0; Mismatches 339;
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14-JUN-2002

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RESULT 15
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                     Thorpe,C., Cahoon,E.B. and Cahoon,R.E. Chlorophyllases
Patent: WO 0229022-A 17 11-APR-2002;
E.I. DU PONT DE NEMOURS AND COMPANY (C
                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum (bread wheat)
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Sequence 17 from Patent
AX411617
AX411617.1 GI:21444167
                 CAACAGTCGCCGGAACTTAICCCGTCGTTTTAITCTTCCATGGCTTTTATCTTCGCAACT 256
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CCAAGGATGCAGGAACCTACCCCGTGGCCATGCTCTTGCACGGCTTCTTCCTCCATAACC
                                                                    CGGTGGATCCGGTGGAAAATGATTCAACAGCACCGCCAAAACCGGTGAGAATCACCTGTC
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/mol_type="unassigned DNA"
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                                                                                                            Score 199; DB 6; Length 1242;
Pred. No. 1.7e-44;
0; Mismatches 350; Indels 2
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Search completed: March 20, 2006, 16:11:51 Job time: 4208.73 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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N	772.8	65.1	796	IJ	BU636473	BU636473
ω	697.4	58.7	699	σ	CB255908	CB255908
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11	413	34.8	413	Ъ	AV561535	AV561535
c 12	412.4	34.7	570	8	DN779181	DN779181
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c 14	391.6	33.0	430	ω	BP605375	BP605375
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	385	32.4	396	_	AV535509	AV535509
	372	31.3	404	_	AV440587	AV440587
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c 20	356.2	30.0	430	ω	BP648469	BP648469
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	BZ290866 SALK 0929	CX046450 UCRCS07_8	CX046588 UCRCS07_9	CX022963 Mdlv4-404	BZ070295 lkj38h09.	CV187182 Mdlv2_401	CL468490 SAIL 1287	BZ292665 SALK_1249	BP655953 BP655953	BP857816 BP857816	CL478965 SAIL 2 F0	BP821899 BP821899	BP833118 BP833118	CL478966 SAIL 2 F0	BP653864 BP653864	BP625285 BP625285	CW836770 ET8513.D8		BP835886 BP835886	BP823922 BP823922	AV563620 AV563620	CX189147 79-E01112

## ALIGNMENTS

source	FEATURES			COMMENT	JOURNAL	TITLE	REFERENCE		TITLE	AUTHORS		SOURCE	KEYWORDS	ACCESSION VERSION	DEFINITION	rocus	RESULT 1
11169 /organism="Arabidopsis thaliana" /mol_type="mRNA"	http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis. Location/Qualifiers	genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full	d M., Cruaud C	The sequences are based on single pass reads.  Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.  Genoscope members carried out semenating and annotation: Castelli	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Web : www represence fre	Genoscope. Direct Submission	2 (bases 1 to 1169)	A Combined Approach to Byainate and improve Arabidopsis Genome Annotation	Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Pull-Length' CDNA Sequences:	<pre>L (bases 1 to 1169) Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,</pre>	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Arabidopsis thaliana (thale cress) Arabidopsis thaliana	DNA.		Arabidop818 thaliana Wili-Length CDNA Complete sequence from clone GSLTFB53ZCO7 of Flowers and buds of strain col-0 of Arabidop8is thaliana (thale cress).	mRNA linear HTC	

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                          ACCGGACTCGGACCGAAGTGGAACAACGTGATGCCACCATGCGCACCAACGGACTTAAAC
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nilarity 86.7%;
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/clone="GSLTFB53ZC07"
/tissue_type="Flowers and b
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/complement(1. .1169)
/gene="At1g19670"
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90 AACTCCGGCGGCTTTTGAGATAGGCAGCCTCCCGACAACCGAGATACCGGTGGATCCGGT 149	30 ATTAICTAGTTTAATACAAATGGCGGCGATAGAGGACAGTCCAACGTTTTCCTCTGTGGT 89	Query Match 65.1%; Score 772.8; DB 5; Length 796; Best Local Similarity 99.5%; Pred. No. 1.9e-215; Matches 786; Conservative 0; Mismatches 2; Indels 2; Gaps 1;	/mol type="mRNA" /ecotype="Columbia" /eb xref="taxon:3702" /db xref="taxon:3702" /db xref="taxon:3702" /clone_lib="Infected Arabidopsis Leaf" /clone="lorgan: Leaf; Vector: pBluescript; Mixed cDNA /note="Organ: Leaf; Vector: pBluescript; Mixed cDNA library of Arabidopsis and E. cichoracearum infected leaf from three weeks old Arabidopsis plants. Plants were harvested 3 days after infection and mRNA oligo dT selected."	Tel: +45 96358467 Fax: +45 98141808 Email: kgw@bio.auc.dk. Location/Qualifiers Location/Qualifiers frce /organism="Arabidopsis thali	¥.		ION BU636473.1 GI:23303728  N BU636473.1 GI:23303728  DS EST.  Arabidopsis thaliana (thale cress)  NISM Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		1012 ATCTTCGTCTAGATTTGTGTTATGTACTA 1040	952 GATCCTTCCGTTTCTCCGGCCAAGCTTGATCCTTCACCTGAGTTGGAAGAAGCTTCTGGT 1011	892 GTTGCGTTTCTCAAGTATAGTTTGTGGGGTGAAAAAGCGGAGATTCGATTGATT	832 ATGTGTAAGAATGGGCAAGGAAAAAAGTCTGAGATGAGGAGCTTTGTAGGTGGAATTGTG 891 	772 GGACATATGGATATGTTGGACGATGATTTGCCCGGTTTTTGTTGGGTTTATGGCCCGGTTGT 831

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                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 699)

Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T., Mitchell-Olds, T. and Weisshaar, B.

Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana Genome Res. 13 (6), 1250-1257 (2003)
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding
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Clone MPIZp772H047Q 5-PRIME, mRNA sequence.
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Insert Length: 699 Std Error: 0.00
Plate: 7 row: H column: 04
Seq primer: T7R; CTAATACGACTCACTATAGGGA.
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                       AAACTGGGCATCGGAAAACCTCAAAGCTCACCAACTTCGGTAAATGCTAATGGAAA
                                                                                GTTGTGCAAATTATTGCCGCCGGGAGGGCAAGTGGAAGTGGAAGTGTGAT
                                                                                                       GTTGTGCAAATTATTGCCGCCGGGAGGGCAAGTGGAAGTGGACGATGCTGGAAGTGTGAT
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T7-Sall-CCACGCGTCGC-5prime-CDNA-polyA-CC-NotI-SP6; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Bstablishment of high-efficiency SNP-based mapping tools and development of Meisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de. This clone is available information."
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/tlssue_type="whole_plant"
/tlssue_type="whole_plant"
/dev_stage="adult_plant, mixed stresses"
/lab_host="s. coli TOP10"
/lab_host="s. coli TOP10"
/clone_lib="MPIZ-ADIS-027"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; cDNA
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BE039090.1 GI:8334106
EST.
Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 715)
Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton
Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton
Ferrea,H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE039090 715 bp mRNA linear AB09E05 AB Arabidopsis thaliana cDNA 5' similar to coronatine-induced protein 1, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bio Sciences West room 513,
Tel: 520-621-7982
Fax: 520-621-1697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Michalowski, C.B. University of Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
     GGTGGGAACCGGACCGAACTGGAACAACGTGATGCCACCATGCGCACCAACGGA
                                                                                   ATCC-GCATATCTTAACGTATAAACCGGA-ATCTTTCGAGCTGGACATACCGGTTGCAGT
                                                                                                                                                        CGTTTTCAGCTCTAATAGGAATTGATCCAGTCGCAGGAACTAACAATACATTAGAACCG
                                                             TTCCGGCATATCTTAACGTATAAACCGGAGATCTTTCGAGCTGGACAAACCGGTTGCAGT
                                                                                                                                     CGTTTT CAGCTTTAATA-GAATTTATCCAGTCGCAGGAACTACCAAATCCATTAGAGCCG
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                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cbm@u.arizona.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                  /ecotype="Columbia"
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/tisue_type="leaves, s
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/clone_lib="AB"
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                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis
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                                                                                                                                                                                                                         51.0%;
                                                                                                                                                                                                          0;
                                                                                                                                                                                                        Score 605.6; DB 2;
Pred. No. 2.7e-166;
0; Mismatches 14;
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                               Email: hxm16@psu.edu
Seq primer: M13 Universal
High quality semisor
                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF773835 563 bp mRNA linear EST 14-APR-2004 AG_FSL_23D02 Arabidopsis ag-1 35S:AG-GR forward subtraction library Arabidopsis thaliana cDNA clone 23D02, mRNA sequence.
CF773835 CF773835 GI:46368801
EST.
                                                                                                                                                                                                                                                                                                  expressed cDNAs in Arabidopsis Plant Mol. Biol. 53 (4), 545-563 (2003)
                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 563)
Hu, W., Wang, Y., Bowers, C. and Ma, H.
                                                                                                                                                                                                                             The Pennsylvania State University 315 Wartik Laboratory, University
                                                                                                                                                                                       Fax: 8148631357
                                                                                                                                                                                                                                                               Hong Ma lab
                                                                                                                                                                                                                                                                                  Contact: Hong Ma
                                                                                                                    POLYA=No.
                                                                                                                                                                                                            Tel: 8148636414
                                                                                                                                                                                                                                                                                                                                      Isolation, sequence analysis,
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/ecotype="Landsberg erecta"
                                                                                             Location/Qualifiers
/db_xref="taxon:3702"
                                                                                                                                   stop:
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1064 197 1004 257 944 317 884 377

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CW836771 681 bp DNA linear GSS 26-NOV-2004 ET8513.Ds5.05.20.01.JU94.b.681 Arabidopsis thaliana Landsberg Ds insertion lines Arabidopsis thaliana genomic clone ET8513, genomic survey sequence.

CW836771
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/tissue_type="Inflorescence lacking open or older flowers"
/dev_stage="4 week old plants"
/clone_lib="Arabidopsis ag-1 35S:AG-GR forward subtraction
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: The pT-Adv vector in the AdvanTAge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 548; DB 6; 1
Pred. No. 2.2e-149;
0; Mismatches 5;
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Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: martiens@cshl.org
This sequence flanks as transposon carrying
line ET8513. The transposon is located within
Class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 516 367 8322
Fax: 516 367 8369
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1 Bungtown Rd., Cold Spring H
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Arabidopsis thaliana
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TTACAAAGAGTGTAAGGCGACGAAAGCCCATTTCGTGGCTGCGGATTACGGACATATGGA
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/clone="ET8513"
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|mol_type="genomic DNA"
|ecotype="Landsberg erecta"
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Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.

A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

DNA Res. 7 (3), 175-180 (2000)

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TCTACTCTGACGTTCTTAACCACATCGCTTCGCATGGTTACATTCTTGTAGCCCCACAGT
                                                               CAGTCGCCGGAACTTATCCCGTCGTTTTATTCTTCCATGGCTTTTATCTTCGCAACTACT
                                                                                    CAGTCGCCGGAACTTATCCCGTCGTTTTATTCTTCCATGGCTTTTATCTTCGCAACTACT
                                                                                                                                            TGGATCCGGTGGAAAATGATTCAACAGCACCGCCAAAACCGGTGAGAATCACCTGTCCAA
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:3702"
/clone="APD27404R"
/tissue_type="aboveground organs"
/tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/clone_lib="Arabidopsis thaliana aboveground organs
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/mol_type="mRNA"
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Biology
University of Waterloo
200, University Ave West,Ontario, C.
Tel: (519) 888-4567 ext 2517
Fax: (519) 746-0614
Email: moffatt@uwaterloo.ca.
Location/Qualifiers
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INT77869.1 GI:62206750

EST.

Thellungiella salsuginea
Thellungiella salsuginea
Thellungiella salsuginea
Eukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Thellungiella.

1 (bases 1 to 741)
Wong, C. E., Li, Y., Whitty, B. R., Diaz-Camino, C., Akhter, S. R.,
Brandle, J. E., Golding, G. B., Weretilnyk, E. A., Moffatt, B. A. and
--iffith M.
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Contact: Moffatt, B
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E5668 [C4091|slt12_e11] Salinity Library Thellungiella salsuginea
cDNA, mRNA sequence.
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GGCTTTTGAGATAGGCAGCCTCCCGACAACCGAGATACCGGTGGATCCGGTGGAAAATGA 158
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                                                                                    TTTAATACAAATGGCGGCGATAGAGGACAGTCCAACGTTTTCCTCTGTGGTAACTCCCGGC 98
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                                                                                                                                            Conservative
                                                                                                                                                                                                                                           /db_xref="taxon:72664"
/tissue_type="Leave"
/dev_stage="4-week old plants"
/clone_lib="Salinity_Library"
/clone_lib="Salinity_Library"
/note="Vector: pcMVSPORT6; Site_1: Not1; Site_2: Sal1;
Library was prepared following The protocol for Invitrogen SuperScript Plasmid System with GAteway Technology for cDNA synthesis and cloning"
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Thellungiella
/mol_type="mRNA"
/cultivar="Yukon"
                                                                                                                                                               44.1%;
                                                                                                                                            0,
                                                                                                                                            Score 524; DB 8; I
Pred. No. 2.7e-142;
0; Mismatches 100;
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19104
Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@atgenome.b
Seq primer: T7
Class: BAC ends
High quality sequence st
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                                                                                                                   BAC End Sequences at ATGC Unpublished (1997)
Other GSSs: T21KB-Sp6
Contact: Ecker J.
Arabidopsis Thaliana Genome
                                                                                                                                                                                                               survey sequence.
B20290
B20290.1 GI:2395344
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T21K8-T7 TAMU Arabidopsis
                                                                                                         University of Pennsylvania
                                                                                                                                                                                                     Feng,J., Dewar,K.,
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="hermaphrodite"
/clone_lib="TAMU"
/note="Vector: BeloBACII;
HindIII; Produced by Rod V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="T21K8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: David Smoller, Ph.D. Genome Systems, Inc., a wholly Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4633 World Parkway Circle, St. Louis, Tel: 877-577-2733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana Gene Expression MicroArray
Unpublished (1999)
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                         AGGATCCTTCCGTTTCTCCGGCCAAGCTTGATCCTTCACCTGAGTTGGAAGAAGCTTCTG
                                                                                                                GTATGTGTAAGAATGGGCAAAGAAAAAAGTCTGAGATGAGGAGCTTTTGTAGGTGGAATTG
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  AGGATCCTNCCGTTTCTCCGGCCAAGCTTGATCTTTCACCTGAGTTGGAAGAAGCTTCTG
                                                                                      TGGTTNNGNTTCTCAAGTANAGTTTNTGGGGTGAAAAAGCGGAGATTCGATTGATTGTGA
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/dev_stage="4 - 7 weeks"
/dev_stage="4 - 7 weeks"
/clone_lib="A. thaliana, Columbia Col-0, root-2"
/clone_lib="A. thaliana, Columbia Col-0, at 4 - 7 weeks.
/note="Wector: pSPRT; Site_1: NotI; Site_2: SalI; cDNA
/library was derived from untreated root tissue from
Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.
Plants were grown in 1:1:1 peat moss/vermiculite/perlite
soil at 22 deg. C +/- 3 deg. C under constant light, and
watered with fertilizer. cDNA synthesis was initiated
using a NotI-oligo(dT) primer. Double-stranded cDNA was
blunted, ligated to SalI adaptors, digested with NotI,
size-selected, and cloned into the NotI and SalI sites of
the pSPORT vector."
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Location/Qualifiers
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|mol_type="mRNA"
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lone="701553812"
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Pred. No. 1.9e-133;
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Best Local Similarity
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AV561535
thaliana
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
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GACATATGGATATGTTGGACGATGATTTGCCCGGTTTTGTTGGGTTTATGGCCGGTTGTA
                                                                                                                                            CCGGACTCGGACCGAAGTGGAACAACGTGATGCCACCATGCGCACCAACGGACTTAAACC
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/tissue type="green siliques"
/clone_Tib="Arabidopsis thaliana green siliques Columbia"
/clone_Tib="Arabidopsis thaliana green siliques Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SQ153b01F"
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/mol_type="mRNA"
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100.0%; Pre
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Pred. No. 1e-109;
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AUTHORS
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Best Local Similarity 85.0
Matches 472; Conservative
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University of Waterloo
200, University Ave West,Ontario,
Tel: (519) 888-4567 ext 2517
Fax: (519) 746-0614
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570 bp mRNA linear EST 05-APR-2005
E7566 [C4680|ssl_fl2] Salinity Subtracted Library Thellungiella
salsuginea CDNA, mRNA sequence.
DN779181
DN779181.1 GI:62208062
EST.
Thellungiella salsuginea
Thellungiella salsuginea
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16021339
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   CTCGGACCGAAGTGGAACAACGTGATGCCACCATGCGCACCAACGGACTTAAACCATGAG 717
                                                                                                                                                                                       CTAATAGGAATTGATCCAGTCGCAGGAACTAACAATACATTAGAACCGATCCGCATATC 597
                                                                 CTCATAGGAATCGACCCGGTAGCAGGAATCAGCAAATGCATGAGAACCGATCCGGAAATC 452
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                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Leave"
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/clone lib="Salinity Subtracted Library"
/clone="Vector: pCMVSPORT6; Site 1: Not1; Site_2: Not1;
/ibrary was prepared following the protocol for BD
Clontech PCR-Select cDNA Subtraction Kit and Promega
pGEM-T Easy Vector System for cDNA synthesis and cloning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Thellungiella
/mol_type="mRNA"
/cultivar="Yukon"
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Pred. No. 1.6e-109;
0; Mismatches 82;
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Thellungiella salsuginea
Thellungiella salsuginea
Thellungiella salsuginea
Embryophyta; Tracheophyta;
Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Thellungiella.
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E7515 [C4629|ss1_b09] Salinity Subtracted Library Thellungiella
salsuginea cDNA, mRNA sequence.
DN779131
                                                                                                                                                                                                                                                                                                                                                                                Department of Biology
University of Waterloo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Griffith, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brandle, J.E.,
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EST.
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(bases 1 to 547)

ng,C.E., Li,Y., Whitty,B.R., Diaz-Camino,C., Akhter,S.R.
andle,J.E., Golding,G.B., Weretilnyk,E.A., Moffatt,B.A.
                                                                                                                                                                                                                                                                                                                         University Ave West, Ontario, (519) 888-4567 ext 2517 (519) 746-0614
                                                                                                                                                                                                                                                                                                     moffatt@uwaterloo.ca.
                                                   /db_xref="taxon:72664"
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/dev_stage="d-week old plants"
/clone_lib="Salinity Subtracted Library"
/clone="Getor: pCMVSPORT6; Site_1: Not1; Site_2: Not1;
/inote="Wector: pCMVSPORT6; Site_1: Not1; Site_2: Not1;
/inoteary was prepared following the protocol for BD
Clontech PCR-Select cDNA Subtraction Kit and Promega
pGEM-T Easy Vector System for cDNA synthesis and clonir
                                                                                                                                                                                                                            /organism="Thellungiella
/mol_type="mRNA"
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   33.9%;
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Length 547
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EST 05-APR-2005

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REFERENCE
AUTHORS
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                                                                   Email: mseki@rtc.riken.go.jp
reversed clone; Please visit our
(http://pfgweb.gsc.riken.go.jp/)
                                                                                                                                                                                   Tel: 81-298-36-4359
                                                                                                                                                                                                   RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
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EST.
                                                                                                                                                                                                                                                                                    Contact: Motoaki Seki
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                                                                                                                                                       Fax: 81-298-36-9060
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Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
                                                                                                            RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibarah
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                     Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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EST.
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                                                                                                                                                                                  Contact: Motoaki Seki
Plant Functional Genomics Research Group
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                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                          and Shinozaki, K.
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/note="Site_1: BamHI; Site_2: SalI; dark-grown"
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/db_xref="taxon:3702"
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/dev_stage="plants at various developmental stages from
/clone_lb="RAFL9"
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/clone_lb="RAFL9"
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Acl35887 Rice stre	Acl35887 Rice stre	Acf83451 Human SIR	Abs53449 cDNA enco	Acl35601 Rice stre	Adq22878 Human sof	Aah34528 Human col	Adl44766 Human ova	Adr84259 Aspergill	Abl32583 Human imm	Ada71938 Rice gene	Adl38382 Human ova	Adi73251 Human ova	Ada71938 Rice gene	Adn60590 Human sec	Adg78299 Human sec	Acd18908 Novel hum	Aax84982 Human sec	Abz15053 Arabidops	Acl27601 Rice abio	Acl32937 Rice abio	Aah41145 Chenopodi	Corn	Aad38081 Wheat chl		Adx50647 Plant ful

ALIGNMENTS

## RESULT 1 AAH41136 20-SEP-1999; 03-APR-2001. JP2001086990-A. Chlorophyllase; transgenic plant; ds. AAH41136 standard; DNA; 1188 20-SEP-1999; Arabidopsis thaliana. Arabidopsis thaliana chlorophyllase coding sequence #1. 21-AUG-2001 AAH41136; (KAGO ) KAGOME KK. (first entry) 99JP-00266181 99JP-00266181. BP

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Query Match 100.0%; Score 1188; Best Local Similarity 100.0%; Pred. No. 0; Matches 1188; Conservative 0; Mismatches

1 GATACATAAATCTTCAACACACTCTTTAATTATCTAGTTTAATACAAATGGCGGCGATA 60

Mismatches

DB 0, 5

Length 1188; Indels

0; Gaps

0

The present sequence is a chlorophyllase protein coding sequence. The chlorophyllase protein coding sequence can be used for the transformation of a plant

Claim 3; Page 10-11; 21pp; Japanese.

DNA encoding chlorophyllase, useful for producing transgenic plants.

P-PSDB; AAB99102. WPI; 2001-338421/36.

Sequence 1188 BP; 327 A; 255 C; 281 G; 325 T; 0 U; 0 Other;

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TTTTCTAGCTCCAAGCTAGCTATTGTTCATGTCCTAAGTTGCATGTGTATTTTATTAAA
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Hirschberg J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel substantially purified nucleic acid molecule encoding a phytol kinase. The nucleic acid molecules and polypeptides of the invention may be useful in mediating tocopherol biosynthesis and in producing plants with increased drought resistance. The current sequence is that of the thale cress chlorophyllase 1 DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thale cress
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biosynthesis and in producing plants with
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05-AUG-2003;
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thale cress; ds; chlorophyllase 1.
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                                                                                     CCGACAACCGAGATACCGGTGGATCCGGTGGAAAATGATTCAACAGCACCGCCAAAACCG
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                            GTGAGAATCACCTGTCCAACAGTCGCCGGAACTTATCCCGTCGTTTTATTCTTCCATGGC
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24-AUG-2000;
26-JAN-2001;
22-JUN-2001;
                                                                                                                                                                                                                                                               WO200216655-A2
                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
Identifying a stress condition to which a producing plants with increased tolerance
                                                                        Harper JF,
                                                                                                                                                                                                      24-AUG-2001;
                                           2002-304127/34.
                                                                                                   SCRIPPS RES INST.
SYNGENTA PARTICIPATIONS
                                                                      Kreps J,
                                                                                                                                             2000US-0227866P
2001US-0264647P
2001US-0300111P
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plant cell has been expose to these abiotic stresses. been exposed and

SEQ ID NO 158; 577pp + Sequence Listing; English

The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office

Sequence 975 BP; 250 A; 222 C; 256 G; 247 T; 0 U; 0 Other;

DB 6;

Length 975;

/ Ma. c Local s. 49 Similarity Conservative 82.1%; Score 975; Pred. No. 0, Mismatches 3.9e-285; Indels 0; 0

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469
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                                                                                                                                                                                                                                                 CCGCCAAAACCGGTGAGAATCACCTGTCCAACAGTCGCCGGAACTTATCCCGTCGTTTTA
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(GLAZ/)
  Glazebrook J,
                                                                     (WANG/)
(DANG/)
(EULG/)
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22-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pathogen infection-related gene; plant; Peronospora parasitica; defence mechanism, RPP7; RRP8; pathogen resistance; transgenic plant; oomycete; fungus; bacterium; virus; nematode; insect; aphid; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #233.
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                                                                   WANG X.
DANGL J L.
EULGEM T.
                                                                                                                                                                 SYNGENTA PARTICIPATIONS UNIV NORTH CAROLINA.
                                                                                                                                         GLAZEBROOK J.
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                                                                                                                                                                                                                                     2000US-0232778P.
2001US-0300183P.
                                                                                                                                                                                                                                                                                                      2001WO-US028506
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Novel isolated polynucleotide, useful for conveying pathogen resistance to plants, and for identifying plants infected with a pathogen.
Claim 3; SEQ ID NO 233; 605pp; English.
                                                                                                                                                                                                                 WPI; 2002-292409/33
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The invention relates to 691 Arabidopsis thaliana genes (ADG87559).

CC ADG87557) whose expression is altered in response to pathogen infection, CC and to homologues of these genes from other plants or fungi, especially CC from maize, soybean, barley, alfalfa, sunflower, canola (oliseed rape), CC cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat. The CC expression of genes of the invention was upregulated or downregulated in CC indicating that they play a role in defence mechanisms. The genes of the CC invention are regulated by RPP7 or RRPB which act via unconventional CC signalling cascades, or by the RPP4-dependent pathway. The invention also CC relates to polypeptides encoded by the pathogen infection-related genes; CC promoter motifs from pathogen infection-related genes; CC plants and their progeny comprising a polynucleotide of identifying a plant cell infected with a pathogen. The cC polynucleotide sequences and methods of the invention are useful for c didntifying plants infected with a pathogen, and for conferring CC resistance to pathogens such as comycetes, fungi, bacteria, viruses, CC neamotodes and insects (e.g., aphids). The present sequence represents an Arabidopsis thaliana gene whose expression is altered in response to CC Peronospora parasitica infection. Note: The sequence data for this patent CC electronic format directly from WIPO at CC. ftp.wipo.int/pub/published\_pct\_sequences.

975 BP; 250 A; 222 C; 256 G; 247 T; 0 U; 0 Other;

Query Match
Best Local Similarity
Matches 975; Conserv Conservative 82.1%; Score 975; DB 6; I 100.0%; Pred. No. 3.9e-285; 0 Mismatches Length 975 Indels 0, Gaps 0

588	TTTTCAGCTCTAATAGGAATTGATCCAGTCGCAGGAACTAACAATACATTAGAACCGAT :	529	ş
480	GGGAAAACGGCGTTTGCGGTTGCGCTAGGCCATGCCGCAACATTAGACCCATCCAT	421	망
528	GGGAAAACGGCGTTTGCGGTTGCGCTAGGCCATGCCGCAACATTAGACCCATCCAT	469	Ş
420	CTACCAACTTCGGTAAATGCTAATGGAAAATACACCTCACTCGTGGGCCACAGCCGCGGT	361	₽
468	CTACCAACTTCGGTAAATGCTAATGGAAAATACACCTCACTCGTGGGCCACAGCCGCGGT	409	ş
360		301	В
408		349	γQ
300	TCGCATGGTTACATTCTTGTAGCCCCCACAGTTGTGCAAATTATTGCCGGCGGGAGGGCAA	241	뮻
348	TCGCATGGTTACATTCTTGTAGCCCCCACAGTTGTGCAAATTATTGCCGCCCGGGAGGGCCAA	289	Ş
240		181	밁
288	-	229	δ
180	CCGCCAAAACCGGTGAGAATCACCTGTCCAACAGTCGCCGGAACTTATCCCGTCGTTTTA 1	121	皮
228	CCGCCAAAACCGGTGAGAATCACCTGTCCAACAGTCGCCGGAACTTATCCCGTCGTTTTA 2	169	Ş
120	TGATTCAACAGCA	61	뭥
168	ATAGGCAGCCTCCCGACAAACCGAGATACCGGTGGATCCGGTGGAAAATGATTCAACAGCA	109	Q
60	ATGGCGGCGATAGAGGACAGTCCAACGTTTTCCTCTGTGGTAACTCCGGCGGCTTTTGAG		뭣
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Novel isolated polynucleotide, useful for conveying pathogen resistance
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                                                                                                                                                                                 Arabidopsis thaliana.
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                                Glazebrook J,
                                                                             (SYGN )
(UYNC-)
(GLAZ/)
                                                                                                                                                                  WO200222675-A2
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                 WPI; 2002-292409/33.
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22-JUN-2001;
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                                              DANGL J L.
EULGEM T.
ZHU T.
                                                                      WANG
                                                                             SYNGENTA PARTICIPATIONS AG. UNIV NORTH CAROLINA. GLAZEBROOK J.
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PT to plants, and for identifying plants infected with a pathogen.

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CC laim 3; SEQ iD NO 32; 605pp; English.

XX

The invention relates to 691 Arabidopsis thaliana genes (ADG87559-CC ADG87557)) whose expression is altered in response to pathogen infection,
CC and to homologues of these genes from other plants or fung; especially
CC from maize, soybean, barley, alfalfa, sunflower, canola (cilseed rape),
CC cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat. The
CC expression of genes of the invention was upregulated or downregulated in
CC Arabidopsis plants infected with the comycete Perconospora parasitica,
indicating that they play a role in defence mechanisms. The genes of the
CC indicating that they play a role in defence mechanisms. The genes of the
CC invention are regulated by RPP7 or RRP8 which act via unconventional so
CC relates to polypeptides encoded by the pathogen infection-related genes,
CC promoter motifs from pathogen infection-related genes (ADG88243-ADG88327)
CC expression cassettes, host cells and pathogen-resistant transgenic
CC plants and their progeny comprising a polynucleotide of the invention;
CC and a method of identifying a plant cell infected with a pathogen. The
polynucleotide sequences and methods of the invention are useful for
CC identifying plants infected with a pathogen, and for conferring
CC resistance to pathogens such as comycetes, fungi, bacteria, viruses,
CC neamotodes and insects (e.g., aphids). The present sequence represents an
Arabidopsis thaliana gene whose expression is altered in response to
CC peronospora parasitica infection. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC printed in the printed specification, but was obtained in

Sequence 975 BP; 250 A; 222 C; 256 G; 247 T; 0 U; 0 Other;

Matches Query Match Best Local Similarity 421 469 361 409 301 349 241 181 229 121 169 109 289 975; 61 49 CCGCATATCTTAACGTATAAACCGGAATCTTTCGAGCTGGACATACCGGTTGCAGTGGTG CTACCAACTTCGGTAAATGCTAATGGAAAATACACCTCACTCGTGGGCCACAGCCGCGGT GTGGAAGTGGATGCTGGAAGTGTGATAAACTGGGCATCGGAAAACCTCAAAGCTCAC TCGCATGGTTACATTCTTGTAGCCCCCACAGTTGTGCAAATTATTGCCGCCGGGAGGGCAA TTCTTCCATGGCTTTTATCTTCGCAACTACTTCTACTCTGACGTTCTTAACCACATCGCT ATAGGCAGCCTCCCGACAACCGAGATACCGGTGGATCCGGTGGAAAATGATTCAACAGCA ATGGCGGCGATAGAGGACAGTCCAACGTTTTCCTCTGTGGTAACTCCGGCGGCTTTTGAG TTTTCAGCTCTAATAGGAATTGATCCAGTCGCAGGAACTAACAATACATTAGAACCGAT CTACCAACTTCGGTAAATGCTAATGGAAAATACACCTCACTCGTGGGCCACAGCCGCGGT GTGGAAGTGGACGATGCTGGAAGTGTGATAAACTGGGCATCGGAAAACCTCAAAGCTTCAC TCGCATGGTTACATTCTTGTAGCCCCACAGTTGTGCCAAATTATTGCCGCCGGGAGGGCAA TTCTTCCATGGCTTTTATCTTCGCAACTACTTCTACTCTGACGTTCTTAACCACATCGCT CCGCCAAAACCGGTGAGAATCACCTGTCCAACAGTCGCCGGAACTTATCCCGTCGTTTTA CCGCCAAAACCGGTGAGAATCACCTGTCCAACAGTCGCCGGAACTTATCCCCGTCGTTTTA Conservative 100.0%; 82.1%; 0; Mismatches Score 975; Pred. No. 3.9e-285; DB 6; **°**; Length 975 Indels 0; Gaps 168 648 540 588 480 528 420 468 360 408 300 228 120 240 288 180 60 0

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                                                                                                                                                                                                              plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance, herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                  Liu
                                                                  (LIUJ/)
(ZHOU/)
(KOVA/)
(SCRE/)
                                                                                                             06-MAY-1999;
05-NOV-2001;
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                                                                                                                                                                                                                                                                                  Plant full length insert polynucleotide seqid
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recombinant DNA construct, useful for improving plant tolerance
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         CGAGCTGGACATACCGGTTGCAGTGGTGGGAACCGGACTCGGACCGAAGTGGAACAACGT
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cold, heat, drought, heats, for conferring drought, herbicides, extreme osmotic conditions, conferring increased resistance to plant disease, pathogens or for or

SEQ ID NO 26342; 15pp; English.

The invention describes a recombinant DNA construct comprising a conjunct consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as comproving plant tolerance to cold, heat, drought, herbicides, extreme commotic conditions, pathogens or pests, for manipulating growth rate in commotic conditions, pathogens or pests, for manipulating growth rate in colls by modification of the cell cycle pathway, for conferring conditions in plant disease, for producing galactomannan, constructed in the recombination of the cell cycle pathway, for conferring condition or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of composition of plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert conjuncted that can be used in the recombinant DNA construct of the

BP; 293 A; 260 Ç 274 G. 298 T; 0 U; 0 Other;

DB 13;

Length 1125;

GGATCCGGTGGAAAATGATTCAACAGCACCGCCAAAACCGGTGAGAATCACCTGTCCAAC AGGAACTAACAAATACATTAGAACCGATCCGCATATCTTAACGTATAAACCGGAATCTTT TGCCGCAACATTAGACCCATCCATCACGTTTTCAGCTCTAATAGGAATTGATCCAGTCGC CACCTCACTCGTGGGCCACAGCCGCGGTGGGAAAACGGCGTTTGCGGTTGCGGTAGGCCA GTGCAAATTATTGCCGCCGGGAGGGCAAGTGGAAGTGGACGATGCTGGAAGTGTGATAAA CGTCGCCGGAACTTACCCCGTCGTCTTATTCTTCCATGGATTCTATCTTCGTAACTACTT AGTCGCCGGAACTTATCCCGGTCGTTTTATTCTTCCATGGCTTTTATCTTCGCAACTACTT CTCTGTGGTAACTCCGGCGGCTTTTGAGATAGGCAGCCTCCCGACAACCGAGATACCGGT 140 AACACACTCTTTTTCCAATATTATACAAATGGCGGGGAAGGAGGACAGTGAGACGTTTTA AACTCTTTAATTATCTAGTTTAATACAAATGGCGGCGATAGAGGACAGTCCAACGTTTTC CACCGCACTCGTGGGCCATAGCCGCGTGGTAAAACCGCGTTTGCGGTTGCGTTAGGCCA CTGGACTTCGAAAACCTCAAAGCTCACCTCCCAAGCTCAGTAAACGCTAATGGCAACTA CTGGGCATCGGAAAACCTCAAAGCTCACCTACCAACTTCGGTXAATGCTAATGGAAAATA GTGCAAGATTTTGCCGCCGGGAGGGCAAGTGGAAGTGGACGATGCTGGAAAAGTGATAAA CTACTCTGATGTTATTAACCACGTAGCTTCTCATGGCTACATTGTTGTAGCCCCACAGCT AGACCCGTCGGCAACCGATTTGACCGCACCTCCAAAGCCTGTAATAATCACCTCCCCAAC CTCGGCGGCAACTCCTTTGGCGTTTGAGTTAGGCAGCCTTCCAACAACCGTGATCCCCGC 130 AGGAATCAGCAAATGCATAAGAACCGATCCCGAAATCTTAACGTACAAACCGGAATCATT CGCCGCAACACTAGACCCATCCATCAAGTTTTCAGCTCTTGTAGGAATAGATCCAGTTGC CTACTCTGACGTTCTTAACCACATCGCTTCGCATGGTTACATTCTTGTAGCCCCACAGTT Conservative 63.0%; 0 Score 748; DB 13 Pred. No. 4e-216; Mismatches 190; Indels ۲ Gaps 70 620 320 200 550 490 500 430 440 370 310 250

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     An isolated polynucleotide encoding a plant chlorophyllase polypeptide, used to produce transformed plants that have controlled induction or postponement of senescence.
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vdblc.pk002.pl9:fis clone"
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                                                                                      GAATTGTGGTTGCGTTTCTCAAGTATAGTTTGTGGGGGTGAAAAAAGCGGAGATTCGATTGA
                                                     GCCTTTTTGTTGCATTCTTGAAGGCTTATTTGGAAGGTCAGACTGGAGATTTCAAAGCCA
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Page 47; 69pp; English.
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The invention relates to plant chlorophyllase (EC 3.1.1.14) proteins and polynuclectides encoding such proteins. Chlorophyllase enzyme is involved in chlorophyllase enzyme is involved in chlorophyllase enzyme is involved in chlorophyllase enzyme is plant cell senescence. Sequences of the invention are used to produce a plant by transforming a plant cell with chlorophyllase and regenerating a plant from the transformed plant cell. They may also be used to transform cells. The plants that are produced can have economical importance as they can allow for the controlled induction or postponement of senescence. The present sequence is grape chlorophyllase cDNA from vdblc.pk002.pl9:fis clone

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987
B₽;
260 A; 224 C; 218 G;
285 T; 0 U;
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 Other;
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Similarity CCCCTCCCAAGCCATTGTTGATTGTTACACCAACCATTCAAGGGACATACCCAGTTCTCT CACCGCCAAAACCGGTGAGAATCACCTGTCCAACAGTCGCCGGAACTTATCCCGTCGTTT 20.2%; milarity 57.6%; Conservative Score 239.4; DB 6; Pred. No. 1.3e-61; 0; Mismatches 336; Indels Length 12; Gaps 85

CGGATTACGGACATATGTATGTTGGACGATGATTTTGCCCCGGTTTTTGTTGGGTTTATGG ACTTAAACCATGAGGAGTTTTACAAAGAGTGTAAGGCGACGAAAGCCCCATTTCGTGGCTG CCGGTTGTATGTGTAAGAATGGGCAAAGAAAAAAGTCTGAGATGAGGAGCTTTGTAGGTG TGGGAACCGGACTCGGACCGAAC---TGGAACAACGTGATGCCACCATGCGCACCAACGG TGCTCCCAGAAAATGTGAAACCAGACCTACTCAAGCTTGCTCTTTCAGGCCACAGCAGAG ACCTACCAACTTCGGTAAATGCTAATGGAAAATACACCTCACTCGTGGGCCACAGCCGCG AAGTGGAAGTGGACGATGCTGGAAGTGTGATAAACTGGGCATCGGAAAAACCTCAAAGCTC CTGAATATGGTCACTTGGACATGTTAGATGATCATCTTTCAGGCTGCATTGGGGCGATTT TTCCCAAAATCCTAACCTATGTTCCTCATTCCTTCAATCTAGCAATCCCAGTTTGCGTAA ATCCGCATATCTTAACGTATAAACCGGAATCTTTCGAGCTGGACATACCGGTTGCAGTGG ACTTCTCAGCCCTACTAGGACTAGACCCTGTTGGTGGGTTGAGTAAATGTTGCCCAAACAG CGTTTTCAGCTCTAATAGGAATTGATCCAGTCGCAGGAACTAACAAATACATTAGAACCG GGGGAAAGACAGCATTTGCTCTGGCACTAGGGTATGC CTTCGCATGGTTACATTCTTGTAGCCCCCACAGTTGTGCAAATTATTGCCGCCGGGAGGGC CGGGTTATATCTGCAAGAGTGGGAAGGGTCCTAGGGACCCCATGAGGAGATGTGTGGGTG TCGGCACGGGGTTGGGCGATGAGCCAAGGAACTGCCTAACATGTCCATGTGCCCCAGATG TGTTTCTTCATGGCTTCGAGCTCCGCAACACCTTCTACACTCAGCTCCTTCAACTCATTT TATTCTTCCATGGCTTTTATCTTCGCAACTACTTCTACTCTGACGTTCTTAACCACATCG TTCAAGAGATCAAATCAGCAGCAGCAGTCACAAATTGGCTATCCTCAGGCCTTCAATCTG CTTCCCATGGATTCATTGTGGTGGCTCCTCAGTTATACCGACTATTACCTCCTTCTGGAA ----TGATACATCCCTCA 676 496 883 616 763 556 646 436 586 376 526 466 406 145 736 703 265 205

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Matches
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                                                                                                                                                                                                                                                                                                                           Sequence 1174 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 52; 69pp; English.
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                       CTTAACCACATCGCTTCGCATGGTTACATTCTTGTAGCCCCACAGTTGTGCAAATTATTG
                                                                                                        TATCCCGTCGTTTTATTCTTCCATGGCTTTTATCTTCGCAACTACTTCTACTCTGACGTT
  CTAGGCCACATAGCTTCACATGGATTCATAATTGTTGCTCCTCAGCTGTGTTGGAGTGTA
                                                                               TACCCTGTAATATTGTTCTGCCATGGATTTTCCCCTTCGCAATAGCTACTACTCTGAGCTC
                                                                                                                                                              AATGCTTCCTCCTCACCTCCAAAACCATTGTTAATCTTTACACCAACCGTGCCTGGCTCA
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llarity 56.9%;
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 ACAACGTGATG----CCACCATGCGCACCAACGGACTTAAACCATGAGGAGTTTTACAAAG
                                                AATCTTTCGAGCTGGACATACCGGTTGCAGTGGTGGGAACCGGACTCGGACCGAAGTGGA
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                                                                                                                                                                                                            TCTCGAAGCTCGCCTTGGCCGGCCACAGCCGAGGAGGCCACACGGCTTTCTCCCTGGCCT
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                             CCTCCTTCGGCATGCCGATGCCGGTGCTGGTCATCGGCACCGGGCTCGGCGAGGAGAAGA
                                                                                        CCGTCGCCGGCACGGGGAAGTCCTCCCAGCTCCAGCCCAAGATCCTCACCTACGAGCCGT
                                                                                                                    CAGTCGCAGGAACTAACAAATACATTAGAACCGATCCGCATATCTTAACGTATAAACCGG
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                                                                                                                                                                    Claim 5; Page 53; 69pp; English
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sflin1.pk002.m10:fis clone"
/EC_number= "3.1.1.14"
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            AAD38079;
                                AAD38079 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1104 BP;
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                                                                                    CTATGGAAGGATTTTGATGCTATTTTAAAGGACCCTAATCTTGCTCCCACTGAAGTCGAT
                                                                                                     GAAAAAGCGGAGATTCGATTGTGAAGGATCCTTCCGTTTCTCCGGCCAAGCTTGAT
                                                                                                                             TTGATGAGAAGGACCACTGGAGGGTTGGTTGTGTCCTTCTTGAGGGCACAATTGAATGAC
                                                                                                                                                  GAGATGAGGAGCTTTGTAGGTGGAATTGTGGTTTGCGTTTCTCAAGTATAGTTTGTGGGGGT
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                                                                                                                                                                                                                                                                                                                                          AAATATTGTAGAACACGTCCTCATATTCTCACTGGCAAGCCACGGTCCTTTGATTTGAAA
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Pred. No. 6.6e-48;
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The invention relates to plant chlorophyllase (EC 3.1.1.14) proteins and polynucleotides encoding such proteins. Chlorophyllase enzyme is involved in chlorophyllage enzyme is involved in chlorophyllage enzyme is involved in chlorophyllage enzyme is involved chlorophyllase enzyme is plant cell senescence. Sequences of the invention are used to produce a plant by transforming a plant cell with chlorophyllase and regenerating a plant from the transformed plant cell. They may also be used to transform cells. The plants that are produced can have economical importance as they can allow for the controlled induction or postponement of senescence. The present sequence is soybean chlorophyllase cDNA from sl2.pkl30.fl5:fis clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An isolated polynucleotide encoding a plant chlorophyllase polypeptide, used to produce transformed plants that have controlled induction or postponement of senescence.
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P-PSDB; AAE23781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1125 BP; 315 A; 219 C; 262 G; 329 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 55; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2001; 2001WO-US031059
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AACGGGCTTCAACCATTGCTTCCCGAGAGCGTTGAAGCCAAACTGGAGAAACTGGTTCTA
                                                        GAAAACCTCAAAGCTCACCTACCAACTTCGGTAAATGCTAATGGAAAATACACCTCACTC 450
                                                                                                                                                                                      TTGCCGCCGGGAGGGCAAGTGGAAGTGGACGATGCTGGAAGTGTGATAAACTGGGCATCG 390
                                                                                                                                                                                                                                                                                                                                                                                                                           TATCCCGTCGTTTTATTCTTCCATGGCTTTTATCTTCGCAACTACTTCTACCTCTGACGTT 273
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                                                                                                                                                                                                                                                                                                                 CTTAACCACATCGCTTCGCATGGTTACATTCTTGTAGCCCCACA---GTTGTGCAAATTA 330
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Pred. No. 5.8e-46;
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                                                                            /*tag= a
/product= "Tulip chlorophyllase
/proc.pk005.d16:fis clone"
/EC_number= "3.1.1.14"
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                                                                                                                      Location/Qualifiers 97. .1107
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Query Match

Sequence

1444 BP;

460 A;

295

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298 ç,

391 7; DB , 6. 0 Ų,

0 Other;

Length 1444;

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The invention relates to plant chlorophyllase (EC 3.1.1.14) proteins and polynucleotides encoding such proteins. Chlorophyllase enzyme is involve in chlorophyll degradation in plant cell sensescence. Sequences of the invention are used to produce a plant by transforming a plant cell with chlorophyllase and regenerating a plant from the transformed plant cell. They may also be used to transform cells. The plants that are produced can have economical importance as they can allow for the controlled induction or postponemant of sensescence. The present sequence is tulip chlorophyllase cDNA from etplc.pk005.d16:fis clone. (Updated on 07-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                          An isolated polynucleotide a used to produce transformed postponement of senescence.
                                                                                                                                                                                                                                                     Claim 5; Page 56-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cahoon EB,
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                                                                                                                                                                                                                                                   69pp; English.
                                                                                                                                                                                                                                                                                                          encoding a plant chlorophyllase polypeptide, i plants that have controlled induction or
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Best Loc Matches Local 756 969 999 909 576 495 456 435 375 336 156 396 Similarity CGTGGCTGCGGATTACGGACATATGGATATGTTGGACGATGATTTGCCCCGGTTTTGTTGG CCCAACGCTTCTACTCCATGCATTCATGCTTCACACACTTTCTACTCTGAGCTTAT TGTTGCTAAGGACTATGGTCACATGGACATGCTAGATGATCATACTGACGGACCTAGAGG GTCATTAGTTATCGGAACAGGTTTAGGTGAATTGAAGAGGAACCTATT---TGCCTGTGC CATTAGAACCGATCCGCATATCTTAACGTATAAACCGGAATCTTTCGAGCTGGACATACC CCCATCCATCACGTTTTCAGCTCTAATAGGAATTGATCCAGTCGCAGGAACTAACAAATA CCACAGCCGCGTGGGAAAACGGCGTTTGCGGTTGCGCTAGGCCATGCCGCAACATTAGA CCTCAAAGCTCACCTACCAACTTCGGTAAATGCTAATGGAAAATACACCTCACTCGTGGG ATGTGATAGTACGAATGGCATCAAGTCTGCTGCAAAAACAACAGATTGGTTGAAGGATGG GCCGGGAGGGCAAGTGGAAGTGGACGATGCTGGAAAGTGTGATAAACTGGGCATCGGAAAA TAACCACATCGCTTCGCATGGTTACATTCTTGTAGCCCCACAGTTGTGCAAATTATTGCC CCCTAAGGGAGTAAATCACCAAGATTTTTACGATGAGTGTTCTTCCCCGTCTTGCCATTT GGTTGCAGTGGGAACCGGACTCGGACCGAAGTGGAACAACGTGATGCCACCATGCGC ACACCAAACCAATCCTCCTGTACTGAATTATATCCCTCACTCTTTGGAACTCAAGATGCC GACTACATTAAGCTTCTCAGCGCTGATCGGGATCGATCCTGTTGACGGAGTACGAAAGGG ACATAGCCGTGGCGCAAAGATGCATTTGCTCTTGCACTAGGATATGC-----GAA ACTGCAAGATGTTCTCCCAACAAAAGTCAGACCAGACCTAAAGAAACTCGGACTGAGCGG CCAGCACATCGCATCCCATGGCTTTATTGTTGTTGTTACCTCAGTTATATCTTGTAGCTAC TCCCGTCGTTTTATTCTTCCATGGCTTTTATCTTCGCAACTACTTCTACTCTGACGTTCT TGATTCAACAGCACCGCCAAAACCGGTGAGAATCACCTGTCCAACAGTCGCCGGAACTTA TGTCTCCGCACCACCTCGGAAGCCACCACTGATCGCAACTCCATTTGAGGAAGGCGAGTA Conservative 15.1%; Score 178.8; Pred. No. 4.1e 0; Mismatches 4.1e-43; ches 357; Indels 15; 434 815 515 755 695 665 635 605 494 455 275 254 782 722

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RESULT 14
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Query Match
Best Local Similarity
Matches 435; Conserv
                                                                                                                       The invention relates to plant chlorophyllase (EC 3.1.1.14) proteins and polynucleotides encoding such proteins. Chlorophyllase enzyme is involved in chlorophyll degradation in plant cell senescence. Sequences of the invention are used to produce a plant by transforming a plant cell with chlorophyllase and regenerating a plant from the transformed plant cell. They may also be used to transform cells. The plants that are produced can have economical importance as they can allow for the controlled induction or postponement of senescence. The present sequence is grape chlorophyllase cDNA from vrllc.pk008.021:fis clone
                                                                                    Sequence 1216 BP;
                                                                                                                                                                                                                                                                                                                                              Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                    An isolated polynucleotide encoding a plant chlorophyllase polypeptide, used to produce transformed plants that have controlled induction or postponement of senescence.
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vrllc.pk008.o21:fis clone"
/EC_number= "3.1.1.14"
/noTe= "CDS does not include start codon"
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                                                                                    331 A; 275 C; 256 G; 354 T; 0 U; 0 Other;
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Score 169.8; DB 6;
Pred. No. 2.1e-40;
0; Mismatches 367;
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                                                                                                                            thaliana chlorophyllase coding
                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                          DNA;
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522 646 582 703

762

819 943 879 586

526

466 411

462

291 406 351

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Query Match 13.8%; Score 163.4; DB 5; Length 1135; Best Local Similarity 54.3%; Pred. No. 1.8e-38; Matches 420; Conservative 0; Mismatches 341; Indels 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1135 BP; 331 A; 233 C; 247 G; 324 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a chlorophyllase protein coding sequence. The chlorophyllase protein coding sequence can be used for the transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 12-14; 21pp; Japanese
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P-PSDB; AAB99103.
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AGAGGGAAGAGTTCTTATTGTTTGTGTAAGAATGGTGA---AGAGAGGAGACCAATGAGG
                                 GTTGGGTTTATGGCCGGTTGTATGTGTAAGAATGGGCAAAGAAAAAAGTCTGAGATGAGG
                                                                                                              CATTTCGTGGCTGCCGGATTACGGACATATGGATTATGTTGGACGATGATTTTGCCCCGGTTTT
                                                                                                                                                                                                        TGCGCACCAACGGACTTAAACCATGAGGAGTTTTACAAAGAGTGTAAGGCGACGAAAGCC 750
                                                                                                                                                                                                                                                                     CCTATACTTGTGATCGGTTCGGGGCTTGGTGAAACCGCTCGGAACCCATTATTCCCCACCG
                                                                                                                                                                                                                                                                                                         GTTGCA---GTGGTGGGAACCGGAACTCGG---ACCGAAGTGGAACAACGTGATGCCACCA 690
                                                                                                                                                                                                                                                                                                                                                        AAACAAACCCCTCCTCCGGTGTTGGCTTACCTTCCAAACTCATTTGACCTAGACAAAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATTCAACAGCACCGCCAAAACCGGTGAGAATCACCTGTCCCAACAGTCGCCGGAACTTAT 216
                                                                                                                                                                                                                                                                                                                                                                                         ATTAGAACCGATCCGCATATCTTAACGTATAAACCGGAATCTTTCGAGCTGGACATACCG 636
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                                                                                    CATTTCGTTGCGAAGGATTATGGGCATTTGGACATGCTTGATGATGATACAAAAGGGATT
                                                                                                                                                                            TGTGCACCTCCCGGAGTGAATCACCGAGAGTTCTTTCGGGAATGTCAAGGTCCAGCATGG
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Search completed: March 20, 2006, 14:14:20 Job time: 704.094 secs

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Result
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USOA_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USOA_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USOA_PUBCOMB.seq:*

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                                                                    Sequence 18, Appl
Sequence 158, App
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5698, Ap	1620, Ap	175209,	18656, A	3830, Ap	556, App	12272, A	5993, Ap	-	60, Appl		60, Appl	60, Appl	2858, Ap	2858, Ap	3821, Ap	94232, A	80160, A	68342, A	27, Appl	166593,	15, Appi

ALIGNMENTS

## NUMBER OF SEQ ID NOS: 79 SOFFWARE: Patentin version 3.2 SEQ ID NO 18 LENGTH: 1188 TYPE: DNA ORGANISM: Synechocystis PCC6803 US-10-634-548-18 S ᅜ 닭 5 S US-10-634-548-18 ; Sequence 18, Application US/10634548 ; Publication No. US20040045051A1 GENERAL INFORMATION: APPLICANT: No. US20040045051Alris, APPLICANT: Lincoln, Kim APPLICANT: Abad, Mark Scott APPLICANT: Eilers, Robert APPLICANT: Hartsuyker, Karen Kindl Query Match 100.0%; Best Local Similarity 100.0%; Matches 1188; Conservative 0; APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Valentin, Henry E. APPLICANT: Venkatesh, Tyamagondlu V. APPLICANT: Venkatesh, Tyamagondlu V. TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof FILE REFERENCE: Ren-01-125 CURRENT APPLICATION NUMBER: US/10/634,548 CURRENT FILING DATE: 2003-08-05 PRIOR APPLICATION NUMBER: us 60/400,689 RRIOR FILING DATE: 2002-08-05 121 121 CCGACAACCGAGATACCGGTGGATCCGGTGGAAAATGATTCAACAGCACCGCCAAAACCG 61 61 GAGGACAGTCCAACGTTTTCCTCTGTGGTAACTCCGGCGGCTTTTGAGATAGGCAGCCTC 1 GATACATAAATCTTCAACACACTCTTTAATTATCTAGTTTAATACAAATGGCGGCGATA 1 GATACATAAATCTTCAACACAACTCTTTAATTATCTAGTTTAATACAAATGGCGGCGATA CCGACAACCGAGATACCGGTGGATCCGGTGGAAAATGATTCAACAGCACCGCCAAAACCG GAGGACAGTCCAACGTTTTCCTCTGTGGTAACTCCGGCGGCTTTTGAGATAGGCAGCCTC Hartsuyker, Karen l Hirshberg, Joseph Karunanandaa, Bala Moshiri, Farhad Stein, Joshua C. 100.0%; Score 1188; 100.0%; Pred. No. 0; Live 0; Mismatches Karen Kindle Balasulojini Sugan B 0 7; Length 1188; Indels 0; Gaps 180 120 120 60 180 0

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GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Warg, Xun
APPLICANT: Chu, Tong
ITILE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 158
JENGTH: 975
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-158
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AACCATGAGGAGTTTTACAAAGAGTGTAAGGCGAAAGCCCATTTCGTGGCTGCGGAT
                                           GGAACCGGACTCGGACCGAAGTGGAACAACGTGATGCCACCATGCGCACCAACGGACTTA
                                                           GGAACCGGACTCGGACCGAAGTGGGAACAACGTGATGCCACCATGCGCACCAACGGACTTA
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APPLICANT: Kreps, Joef
APPLICANT: Kreps, Joef
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
ITILE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
ITILE OF INVENTION: STRESS-REGULATED SOF USE
ITILE OF INVENTION: STRESS-REGULATED SOF USE
ITILE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NO 158
SEQ ID NO 158
LENGTH: 975
TYPE: DNA
ORGANTSM: Arabidonnis thaliana
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US-09-938-842A-158
; Sequence 158, Application US/09938842A
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; GENERAL INFORMATION:
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US-10-425-114-26342
US-10-425-114-26342
Sequence 26342, Application US/10425114
Publication No. US/20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5331)B
CURRENT PLING DATE: 2003-04-28
UNMBER OF SEQ ID NOS: 73128
SEQ ID NO 26342
LENGTH: 1125
TYPE: DNA
ORGANISM: Brassica napus
FEATURE:
CTHER INFORMATION: Clone ID: LIB4156-010-D3_FLI
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                                                                                    TGAAAAAGCGGAGATTCGATTGATTGTGAAGGATCCTTCCGTTTCTCCGGCCAAGCTTGA
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   TCCTTTGCCGGAGCTGGAAGAGGCTTCTGGTTATCTCGTCTAGATTTGTGGTTAAGGAAT 1029
                                                                TGAAAAGTCAGAGATTCGACAGATTGTGAAGGATCCCTCTGTTTCTCCGGCGAGGCTTGA
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Pred. No. 4e-216;
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Publication No. US20050081263A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Comps
TITLE OF INVENTION: Chlorophyllases
FILE REFERENCE: BB1477 PCT
CURRENT APPLICATION NUMBER: US/10/381,123
CURRENT FILING DATE: 2003-03-21
FRIOR APPLICATION NUMBER: PCT/US01/31059
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-0-05
IPRIOR APPLICATION NUMBER: 60/238,161
PRIOR FILING DATE: 2000-10-05
INUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 987
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US-10-381-123-1
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US-10-381-123-1
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Best Local Sim:
Matches 473;
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 CGGATTACGGACATATGGATATGTTGGACGATGATTTGCCCCGGTTTTGTTGGGTTTATGG
                                 GAGTGAACCATGTAGAGTTTTTCAGTGAGTGTAAACCTCCTTGTTCCCACTTTGTGACTA
                                                                  ACTTAAACCATGAGGAGTTTTACAAAAGAGTGTAAGGCGACGAAAGCCCATTTCGTGGCTG 763
                                                                                                                      TGGGAACCGGACTCGGACCGAAG----TGGAACAACGTGATGCCACCATGCGCACCAACGG
                                                                                                                                                               TTCCCAAAATCCTAACCTATGTTCCTCATTCCTTCAATCTAGCAATCCCAGTTTGCGTAA
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ilarity 57.6%;
Conservative
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Pred. No. 2e-61;
0; Mismatches 336;
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PRIOR APPLICATION UNMBER: 60/238,161
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
LENGTH: 1174
TYPE: DNA
ORGANISM: Glycine max
US-10-381-123-7
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US-10-381-123-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 17.1%;
Best Local Similarity 56.9%;
Matches 480; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: E.I. du Pont de Nemours and Company TITLE OF INVENTION: Chlorophyllases FILE REFERENCE: BB1477 PCT CURRENT APPLICATION NUMBER: US/10/381,123 CURRENT FILING DATE: 2003-03-21 PRIOR APPLICATION NUMBER: PCT/US01/31059 PRIOR FILING DATE: 2001-10-04
                                                                                                                                                                  402
                                                                                                                                                                                                                                               342
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                                                                                                          GCAACATTAGACCCATCCATCACGTTTTCAGCTCTAATAGGAATTGATCCAGTCGCAGGA 564
                                                                                                                                                                                                                                                                            GCATCGGAAAACCTCAAAGCTCACCTACCAACTTCGGTAAATGCTAATGGAAAATACACC 444
                                                                                                                                                                                                                                                                                                                                                  CCGCC-----GGGAGGGCAAGTGGAACTGGAACGATGCTGGAAAGTGTGATAAACTGG--- 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACCCTGTAATATTGTTCTGCCATGGATTTTCCCTTCGCAATAGCTACTACTCTGAGCTC
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                                                                                                                                                                                      TCACTGGTGGGCCACAGCCGCGGTGGGAAAAACGGCGTTTGCGGTTGCGCTAGGCCATGCC 504
    CCATGTAAATCTTGCGAAACATTTCCTCCTATTCTCACTGGCATGTCCCAATCCTTCAAT
                                       ACTAACAAATACATTAGAACCGATCCGCATATCTTAACGTATAAACCGGAATCTTTCGAG 624
                                                                                                                                                              GTTTTATCAGGTCACAGCAAGGGTGGCAAAACTGTATTTGCTGTGGCACTTGGTTATGCT
                                                                                                                                                                                                                                        GCCGAGGAGGGCTTCAACCTCTGCTTCCAGAGAATGTTGAAGCCAAATTGGATAAATTG 401
                                                                                                                                                                                                                                                                                                                       CGGTCTATGTTGGAACCTGGTGATGAAGTTAAATTTGCAGGGAAAGTTGTGGATTGGCTA 341
                                                                                                                                                                                                                                                                                                                                                                                                    CTAGGCCACATAGCTTCACATGGATTCATAATTGTTGCTCCTCAGCTGTGTTGGAGTGTA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTAACCACATCGCTTCGCATGGTTACATTCTTGTAGCCCCACAGTTGTGCAAATTATTG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATCCCGTCGTTTTATTCTTCCATGGCTTTTATCTTCGCAACTACTTCTACTCTGACGTT 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGGTTGTATGTGTAAGAATGGGCAAAGAAAAAGTCTGAGATGAGGAGCTTTGTAGGTG
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                                                                                 0;
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Pred. No. 3.5e-50;
0; Mismatches 339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1174;
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APPLICANT: E.I. du Pont de Nemours and Company
ITILE OF INVENTION: Chlorophyllases
FILE REFERENCE: BB1477 PCT
CURRENT APPLICATION NUMBER: US/10/381,123
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: PCT/US01/31059
PRIOR PILING DATE: 2001-10-04
PRIOR PILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR PILING DATE: 2000-10-05
NUMBER OF ESO ID NOS: 30
SOFTWARE: Microsoft Office 97
SEO ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 1242
; TYPB: DNA
; ORGANISM: Triticum aestivum
US-10-381-123-17
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US-10-381-123-17
; Sequence 17, Application US/10381123
; Publication No. US20050081263A1
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Best Local Similarity 55.8%;
Matches 476; Conservative
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  TGATAAACTGGGCATCGGAAAACCTCAAAGCTCACCTACCAACTTCGGTAAATGCTAATG
                                                                                                                    ACTICTACGAACACCTTCTCCGGCACGTCGCATCCCACGGCTTCATCATTGTCGCGCCCCC
                                                                                                                                                         ACTTCTACTCTGACGTTCTTAACCACATCGCTTCGCATGGTTACATTCTTGTAGCCCCAC
                                                                                                                                                                                                                        CAACAGTCGCCGGAACTTATCCCGTCGTTTTATTCTTCCATGGCTTTTATCTTCGCAACT
                                                                                                                                                                                                                                                                              CGATTCAGGTGGATGAGAATGCGGCGCCGACACCACCGATCCCGGTGCTGATCGTCGCAC
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                                       AGTTCAGCATCAGTATCATACCTTCGGGTGACGCAGAGGACATCGCCGCGGCAGCCAAGG
                                                                            AGTTGTG---CAAATTATTGCCGCCGGGAGGGCCAAGTGGAAGTGGACGATGCTGGAAGTG
                                                                                                                                                                                                   CCAAGGATGCAGGAACCTACCCCGTGGCCATGCTCTTGCACGGCTTCTTCCTCCATAACC
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                                                                                                                                                                                                                                                                                                                                                         Score 199; DB 9; Pred. No. 4.5e-49; O; Mismatches 350;
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                                                                                                                                                                                                                                                                                                                                                             Indels
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872

918 812 858

752

692

27;

Gaps

433 392 373

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APPLICANT: E.I. du Pont de Nemours and Company TITLE OF INVENTION: Chlorophyllases FILE REFERENCE: BB1477 PCT
CURRENT APPLICATION NUMBER: US/10/381,123
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: PCT/US01/31059
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 9
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                                                                                                                                             ; TYPE: DNA
; ORGANISM: Glycine
US-10-381-123-9
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US-10-381-123-9
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/10381123 Publication No. US20050081263A1 GENERAL INFORMATION:
                                                                       Query Match
Best Local Similarity
Matches 473; Conserv
                                                                                                                                                                                                 LENGTH: 1104
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     113
                             154 AATGATTCAACAGCACCGCCAAAACCGGTGAGAATCACCTGTCCCAACAGTCGCCGGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           972
     AGTGCTTCCTCACCTCCAAAACCATTGCTAATTTTTACACCAACTGTTCCTGGCGCA
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nilarity 56.3%;
Conservative
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                                                                       Score 194.4; DB 9;
Pred. No. 1e-47;
0; Mismatches 346;
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APPLICANT: B.I. du Pont de Nemours and Company
TITLE OF INVENTION: Chlorophyllases
FILE REFERENCE: BB1477 PCT
CURRENT APPLICATION NUMBER: US/10/381,123
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: PCT/US01/31059
PRIOR FILING DATE: 2001-10-04
PRIOR PLICATION NUMBER: 60/238,161
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 11
LENGTH: 1125
TYPE: DNA
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US-10-381-123-11
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RESULT 10
US-10-424-599-45715
; Sequence 45715, Application US/10424599
; Publication No. US20040031072A1
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llarity 56.6%;
Conservative
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Pred. No. 9.4e-46;
0; Mismatches 340;
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; OTHER INFORMATION: US-10-424-599-45715
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE REFERENCE: 38-21(53223)B
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 45715
LENGTH: 1307
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ORGANISM: Glycine
FEATURE:
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476; Conserv
GTCTGAGATGAGGAGCTTTGTAGGTGGAATTGTGGTTTGCGTTTCTCAAGTATAGTTTGTG
                                                                                          GCCCGGTTTTGTTGGGT----TTATGGCCGGTTGTATGTGTAAGAATGGGCAAAGAAAAAA
                                                                                                                                                                                            GACGAAAGCCCATTTCGTGGCTGCGGATTACGGACATATGGATATGTTGGACGATGATTT
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nilarity 56.4%;
Conservative
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Pred. No. 7.3e-45;
O; Mismatches 343;
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Sequence 13, Application US/10381123

Publication No. US20050081263A1

GENERAL INFORMATION:
APPLICAMY: E.I. du Pont de Nemours and Company
ITILE OF INVENTION: Chlorophyllases
FILE REFERENCE: BB1477 PCT
CURRENT APPLICATION NUMBER: US/10/381,123
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: PCT/US01/31059
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 13
LENGTH: 11444
TYDE: NUM
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US-10-381-123-13
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ORGANISM: Gesneriana
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Local Similarity 54.1%;
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ACCAACGGACTTAAACCATGAGGAGTTTTTACAAAGAGTGTAAGGCGACGAAAGCCCATTT
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                                          GTCATTAGTTATCGGAACAGGTTTAGGTGAATTGAAGAGGAACCTATT---TGCCTGTGC
                                                                                      GGTTGCAGTGGTGGGAACCGGACTCGGACCGAAGTGGAACAACGTGATGCCACCATGCGC
                                                                                                                                   ACACCAAACCAATCCTCCTGTACTGAATTATATCCCTCACTCTTTGGAACTCAAGATGCC
                                                                                                                                                                                                                        GACTACATTAAGCTTCTCAGCGCTGATCGGGATCGATCCTGTTGACGGAGTACGAAAGGG
                                                                                                                                                                                                                                                                  CCCATCCATCACGTTTTCAGCTCTAATAGGAATTGATCCAGTCGCAGGAACTAACAAATA 575
                                                                                                                                                                                                                                                                                                                 ACATAGCCGTGGCGCAAAGATGCATTTGCTCTTGCACTAGGATATGC------GAA
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Pred. No. 6.8e-43;
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Publication No. US20050081263A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
TITLE OF INVENTION: Chlorophyllases
FILE REFERENCE: BB1477 PCT
CURRENT APPLICATION NUMBER: US/10/381,123
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: PCT/US01/31059
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR APPLICATION NUMBER: 90/238,161
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 30
SOFTWARB: Microsoft Office 97
SEQ ID NO 3
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; ORGANISM: Vitis
US-10-381-123-3
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US-10-381-123-3
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                         CGTTTTCAGCTCTAATAGGAATTGATCCAGTCGCAGGAACTAACAAATACATTAGAACCG 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTAGGTGGAATTGTGGGTTGCGTTTCTCAAGTATAGTTTGTGGGGTGAAAAAAGCCGAGAGT
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GAGGCAAAACTGCTTTTGCTCTAGCACTGAG-----AAAAAGCATCCACTTCTCTGA
                                                                                                                              TACTTCCTCCCCATGTTCGGCCAAATTTAAGCAAACTAGGACTTGCCGGCCATAGTCGTG 411
                                                                                                                                                                                                                        ACCTACCAACTTCGGTAAATGCTAATGGAAAATACACCTCACTCGTGGGCCACAGCCGCG 466
                                                                                                                                                                                                                                                                       GCGAAGAGATCAAGTCCGCAGCTGCTTTAACAAATTGGTTATCCAAAGGACTCCATGACT 351
                                                                                                                                                                                                                                                                                                                                                             CCTCTCATGGTTTCATTGTTCTTGCTCCTCAGTTATACACTGTGGCTGGACCAGATTCAA 291
                                                                                                                                                                                                                                                                                                                                                                                                          CTTCGCATGGTTACATTCTTGTAGCCCCACAGTTGTGCAAATTATTGCCCGCCGGGAGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCCTCCACTGCAACTCTTGATTGCTACGCCCTCTGAAGCAGGGGAGTTCCCGCTGCTGC 171
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Pred. No. 3.4e-40;
0; Mismatches 367;
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; SEQ ID NO 19
; LENGTH: 1135
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-634-548-19
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US-10-634-548-19
; Sequence 19, Application US/10634548
; Publication No. US20040045051A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: Ren-01-125
CURRENT APPLICATION NUMBER: US/10/634,548
CURRENT FILING DATE: 2003-08-05
PRIOR APPLICATION NUMBER: US 60/400,689
PRIOR FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: No. US20040045051Alris, Susan APPLICANT: Lincoln, Kim APPLICANT: Abad, Mark Scott APPLICANT: Eilers, Robert APPLICANT: Hartsuyker, Karen Kindle APPLICANT: Hirshberg, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Stein, Joshua C.
APPLICANT: Valentin, Henry E.
APPLICANT: Venkatesh, Tyanagondlu V.
TITLE OF INVENTION: Tocopherol biosynthesis
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APPLICANT:
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                                                                                                                                                                                                              Similarity
AACCACATCGCTTCGCATGGTTACATTCTTGTAGCCCCACAGTTGTGCAAATTATTGCCG
                                                              CCCGTCGTTTTATTCTTCCATGGCTTTTATCTTCGCAACTACTTCTACTCTGACGTTCTT
                                                                                                                  GATTCAACAGCACCGCCAAAACCGGTGAGAATCACCTGTCCAACAGTCGCCGGAACTTAT
                                      CCGGTGGTGATGCTCCTCCATGGTTACCTTCTCTACAACTCCTTCTATTCTCAGCTTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTAAACCATGAGGAGTTTTTACAAAGAGTGTAAGGCGACGAAAAGCCCATTTCGTGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ellers, Robert
Hartsuyker, Karen Kindle
Hirshberg, Joseph
Karunanandaa, Balasulojini
Moshiri, Farhad
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                                                                                                                                                                                              Conservative
                                                                                                                                                                                                          13.8%;
                                                                                                                                                                                        Score 163.4; DB 7;
Pred. No. 2.9e-38;
0; Mismatches 341;
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154 AATGATICAACAGCACCGCCAAAACCGGTGAGAATCACCTGTCCAACAGTCGCCGGAACT

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NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 34940
LENGTH: 1068
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
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US-10-424-599-34940
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                                                                              US-10-424-599-34940
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34940, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                    Best Local
                                     Query Match
                                                                                                                                                                                                                          APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21(5322))B
FURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa Thomas J APPLICANT: Kovalic David K
                                                                                          OTHER INFORMATION: Clone ID: PAT_MRT3847_131553C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         808
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    447;
                    Similarity
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Score 135.6; DB 7;
Pred. No. 7.9e-30;
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Sequence 25, Application US/10381123
Publication No. US20050081263A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Compa
TITLE OF INVENTION: Chlorophyllases
FILE REFERENCE: BB1477 PCT
CURRENT APPLICATION NUMBER: US/10/381,123
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: PCT/US01/31059
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-05
INUMBER OF SEQ ID NOS: 30
SOPTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 1156
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US-10-381-123-25
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                                                             14:42:17
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1: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*

12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-330-773-664

6 US-09-925-065A-308174

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US-09-925-065A-683561

US-09-925-065A-102394

US-09-925-065A-92249

US-09-925-065A-92549

US-09-925-065A-158029

US-09-925-065A-106455

US-09-925-065A-106459

US-09-925-065A-106454

US-09-925-065A-106454

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US-10-240-708-29
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5830.519 Million cell updates/sec
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                           Sequence 29, Appl
Sequence 1, Appli
Sequence 881350,
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Sequence 46341, A
Sequence 38673, A
Sequence 38673, A
Sequence 38673, A
Sequence 38673, A
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Sequence 683561,
Sequence 102394,
Sequence 849244,
Sequence 902549,
Sequence 358029,
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US-10-995-561-51601	US-10-750-623-63067	US-10-750-185-63067	US-09-925-065A-279572	US-09-925-065A-257742	US-10-330-773-374	US-10-330-773-395	US-11-136-527-134	US-11-136-527-4230	US-09-925-065A-655069	US-09-925-065A-383958	US-09-925-065A-256291	US-11-098-686-8739	US-10-995-561-13227	US-10-240-708-93	US-10-932-182A-2957	US-10-932-182A-2957	US-10-750-623-52094	US-10-750-185-52094	US-11-098-686-9335	US-10-775-169-78	US-10-995-561-22763	US-10-793-626-4133	US-10-793-626-4106	US-11-096-568A-1623
51601,		Sequence 63067, A	Sequence 279572,	Sequence 257742,	Sequence 374, App	Sequence 395, App	Sequence 134, App	Sequence 4230, Ap	Sequence 655069,	Sequence 383958,	Sequence 256291,	Sequence 8739, Ap	Sequence 13227, A	Sequence 93, Appl	Sequence 2957, Ap	Sequence 2957, Ap	Sequence 52094, A	Sequence 52094, A	Sequence 9335, Ap	Sequence 78, Appl	Sequence 22763, A	Sequence 4133, Ap	Sequence 4106, Ap	Sequence 1623, Ap

## ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT FAPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/252,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2000-01-1-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/269,846

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOPTWARE: PastSEQ for Windows Version 4.0

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, Sequence 175209, Application US/09925065A
, Publication No. US20040181048A1
, GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                         Query Match 3.3%;
Best Local Similarity 56.0%;
Matches 75; Conservative
1175 AAAAAAAAAAAAA 1188
                                                                                                          1115 TAAGTTGCATGTGTATTTTATTAAACTCGATCAAAACATTTGTTATAGTTTTTACCCCAA 1174
                                                                                                                                                                                                                           324 CATGITCAGICTTTATTCTGGCAAAACACAATGAAAGGTTTTTT
                                                                                                                                                                            384 TTTÁTGATTTGÁGÁÁÁATTTCATTTTTAAAGÁTAATGÁÁTTTÁGCTCTTCCGCTAGGGC
                                                                                                                                                                                                                                                                         Score 39.6; D
Pred. No. 1.1;
0; Mismatches
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RESULT 2
US-09-25-065A-683561/c
US-09-25-065A-683561, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
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US-09-925-065A-102394
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                   PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR PELICATION NUMBER: US 60/252,147
PRIOR PELICATION NUMBER: US 60/252,147
PRIOR PELICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR PELICATION NUMBER: US 60/261,766
PRIOR PELICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
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PRIOR FILING DATE: 2000-10-24
PRIOR PELICATION NUMBER: US 60/252,147
PRIOR PELICATION NUMBER: US 60/252,147
PRIOR PELICATION NUMBER: US 60/250,092
PRIOR PELICATION NUMBER: US 60/261,766
PRIOR PELICATION NUMBER: US 60/261,766
PRIOR PELICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 102394, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 113;
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                           APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08
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Local Similarity 47.7%;
APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          854 AAAAGTCTGAGATGAGGAGCTTTGTAGGTGGAATTGTGGTTGCGTTTCTCAAGTATAGTT 913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
NUMBER: US 60/289,846
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; PRIOR FILING DATE: 2001-05-09; NUMBER OF SEQ ID NOS: 957086; SOFTWARE: FastSEQ for Windows Ve; SEQ ID NO 102394; LENCTH: 534; TYPE: DNA ; ORGANISM: Homo sapiens US-09-925-065A-102394
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FILE OF INVESTIGNAL
FILE OF INVESTIGNAL
FILE OF INVESTIGNAL
FILE OF INC DATE: 2001-08-08
FRIOR APPLICATION NUMBER: US 60/243,096
FRIOR APPLICATION NUMBER: US 60/252,147
FRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
FRIOR APPLICATION NUMBER: US 60/252,147
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-05-09
FRIOR APPLICATION NUMBER: US 60/289,846
FRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
FROR IND 849244
FENCETTI- 543
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                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-849244
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US-09-925-065A-849244
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                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Best Local (
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
1008 TGGTATCTTCGTCTAGATTTGTGTTATGTACTATTATCAGAGGGGTCTTGAATATTTGAA 1067
                                                                148
                                                                                                        948 GAAGGATCCTTCCGTTTCTCCGGCCAAGCTTGATCCTTCACCTGAGTTGGAAGAAGCTTC 1007
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                                                                                                                                                  TGACTTTGGGATTTTCCÁGTÁCGGCCCGTGGAGAGCCTCÁAAGGÁTÁTATCCCTCÁTAAT 147
                                                                                                                                                                                         TTATATATTTGACAAACTTCCCCCAAATTGAATTCTAAATTAAGTATTTTTGACCTAGAAT 87
                                                                                                                                                                                                                                                                           TTGTATGTGTAAGAATGGGCAAAGAAAAAAGTCTGAGATGAGGAGCTTTGTAGGTGGAAT 887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTTGTGTTATTGTTACATGGCCTTTATTTAAATGTGTAAAATGCCTAAAGCCTTTTTCT 388
                                                                GCAGAGATGTTAAGTTAATCAAGCTTGTTTGATGTGTAATTGTATGGGAAGTATTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCACATCGCTTCGCATGGTTACATTCTT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCATACCACCAGTATTAGCACTTTAAAC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCAACAGCACCGCCAAAACCGGTGAGAATCACCTGTCCAACAGTCGCCGGAACTTATCC 218
                                                                                                                                                                                                                                                                                                                     3.2%;
ilarity 46.5%;
Conservative
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Pred. No. 3.8;
0; Mismatches 139;
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Pred. No. 3.
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Sequence 358029, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.

ITITLE OF INVENTION: Identification and Mapping of Single
ITITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/289,846
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US-09-925-065A-358029
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US-09-925-065A-902549/c
; Sequence 902549, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-925-065A-902549
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Best Local Similarity 51.5%;
Matches 86; Conservative
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PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1075 TCAATGTTTTCTAGCTCCAAGCTAGCTATTGTTCATGTCCTAAGTTGCATGTGTATTTTT 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1015 ТТССТСТАСАТТТСТСТТАТСТАСТАТТАТСАСАСССССТТСАЛАТАТТТСАЛАЛАССТА 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTGTGCCCTGAAAATATATTTGATATAGTTTTTATTTTAAAAAAA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAATTTCCATGTATTTGTACAATTTCCAGTGTTCTTGTTATTGATTTCTTGTTTATTCT
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; ORGANISM: Homo sapiens
US-09-925-065A-106455
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-358029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 106455
LENGTH: 590
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NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows
SEQ ID NO 358029
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Best Local Similarity
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Best Local
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
1122 CATGTGTATTTTATTAAACTTCGATCAAAACATTTGTTATAGTTT 1166
                                                                                                                                        1065 GAAAAACCTATCA---ATGTTTTCTAGCTCCAAGCTAGCTATTGTTCATGTCCTAAGTTG 1121
                                                                                                                                                                                                                                            1005 TTCTGGTATCTTCGTCTAGATTTGTGTTATGTACTATTATCAGAGGGGTCTTGAATATTT 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1017 CGTCTAGATTTGTGTTATGTACTATTATCAGAGGGGTCTTGAATATTTGAAAAACCTATC
                                                                                   365 TAAATATATATACAGTAGTTCCCCCTTATCCTAGGGAGATATGTTCCAAGACCCCTAGTG
                                                                                                                                                                                          305 TCCTTTTAACTTTGTGTGGATTTTTGTTGTCTCCTATTTTCTTATAGGTGTTGATAAATC
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                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                          Score 37; DB 6;
Pred. No. 5.7;
                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                 70;
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                                                                                                                                                                                                                                                                                                                                                Length 590
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PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR PPLICATION NUMBER: US 60/252,147
PRIOR PPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-20
PRIOR PPLICATION NUMBER: US 60/250,092
PRIOR PPLICATION NUMBER: US 60/261,766
PRIOR PPLICATION NUMBER: US 60/261,766
PRIOR PPLICATION NUMBER: US 60/261,766
PRIOR PPLICATION NUMBER: US 60/289,846
PRIOR PPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-05-09
NUMBER OF SED ID NOS: 957086
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41521
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US-09-925-065A-106454
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; Sequence 417521, Application US/09925065A
; Publication No. US20040181048A1
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                                     CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR PRIOR DATE: 2001-136
PRIOR PRIOR DATE: 2001-01-16
PRIOR PRIOR DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: Wang, Da
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    SEQ ID
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 594
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                       FastSEQ for Windows Version 4.0
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Pred. No. 5.7;
0; Mismatches
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RESULT 11
US-10-240-708-29
; Sequence 29, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-106454
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US-09-925-065A-283413/c
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Best Local
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ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOPTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 283413
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 108827.135
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                                   TAAGTTGCATGTGTATTTTATTTAAACTCGATCAAAACATTTGTTATAGTTTT 1167
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TTCTGTTGTTTTTTTTTTCCTCTTGGTCTAGCTAAAGGTATTTTATTATATATT
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Pred. No. 6
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Pred. No.
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0; Mismatches
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RESULT 12
US-11-091-018-1
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                                                                          CURRENT APPLICATION NUMBER: US/11/091,018
CURRENT FILING DATE: 2005-03-25
PRIOR APPLICATION UNMBER: PCT/US03/29906
PRIOR FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 10/255,120
PRIOR FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 10/419,723
PRIOR APPLICATION NUMBER: 10/419,723
PRIOR APPLICATION UNMBER: 10/650,120
PRIOR FILING DATE: 2003-08-27
PRIOR FILING DATE: 2003-08-27
PRIOR FILING DATE: 2003-08-27
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Publication No. US20050287551A1
GENERAL INFORMATION:
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Best Local Similarity 47.3%;
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APPLICANT: Thorleifsson, Gudmar
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
TITLE OF INVENTION: METHODS OF TREATMENT
FILE REFERENCE: 2345.2010-016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
1EQ ID NO 29
LENGTH: 5666
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PRIOR TILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: 10/067,514
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 09/811,352
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CURRENT FILING DATE: 2002-10-03
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PRIOR FILING DATE: 2001-04-06
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8; Length 5666;
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human G
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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FRATURE:
FRATURE
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Matches
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SEQ ID NO 881350
LENGTH: 617
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1
LENGTH: 1691140
TYPE: DNA
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Publication No. US20040181048A1
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ilarity 50.6%;
Conservative
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ilarity 56.8%;
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Pred. No. 2.5e+02;
0; Mismatches 51;
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RESULT 14 US-10-750-185-46341/c

Sequence 46341, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:

INC.

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PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOPTWARE: PatentIN version 3.1
SEQ ID NO 46341
LENGTH: 1462
TYPE: DNA
RCANISM: Bovine 19866880447381
US-10-750-623-46341
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; SEQ ID NO 46341
; LENGTH: 1462
; TYPE: DNA
; ORGANISM: Bovine 198668804472
US-10-750-185-46341
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US-10-750-623-46341/c
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: LOENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
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Best Local Similarity
Matches 99; Conserv
  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                            APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR
FILE REFERENCE: MMII1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILION-2003-12-31
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
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PRIOR FILING DATE: 2002-12-31
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    Score 36;
Pred. No.
DB
16;
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                       Length 1462;
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Search completed: March 20, 2006, 14:23:26 Job time: 477.098 secs
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Minimum DB
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Perfect score:
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Maximum Match 100%
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seq length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents NA:*

1: /cgn2_6/ptcodata/l/ina/1_COMB.seq:*

2: /cgn2_6/ptcodata/l/ina/5_COMB.seq:*

3: /cgn2_6/ptcodata/l/ina/6A_COMB.seq:*

4: /cgn2_6/ptcodata/l/ina/6B_COMB.seq:*

5: /cgn2_6/ptcodata/l/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptcodata/l/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptcodata/l/ina/PCOMB.seq:*

8: /cgn2_6/ptcodata/l/ina/RE_COMB.seq:*

9: /cgn2_6/ptcodata/l/ina/RE_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is the number of results predicted by chance to have a ster than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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1188
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                                           3.5 7218
3.1 601
3.1 161900
3.1 161901
3.1 100836
3.1 100837
3.1 100837
3.1 317368
3.0 406
3.0 4249
3.0 4249
3.0 3769
3.0 3769
3.0 862
2.9 862
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-949-016-12001
US-09-949-016-16001
US-09-949-016-17000
US-09-949-016-17000
US-09-949-016-17000
US-09-949-016-17000
US-09-949-016-173353
US-09-949-016-13353
US-09-949-016-13353
US-09-10-279-4133
US-09-10-279-4133
US-09-10-279-4133
US-09-10-279-4133
US-09-10-279-4133
US-09-434-940-5
US-09-434-940-5
US-09-434-940-5
US-09-622-254B-24
US-09-622-254B-24
US-09-621-976-2813
US-09-621-976-2813
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Million cell updates/sec
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                   Sequence 14, Appl Sequence 41157, A Sequence 41157, A Sequence 12685, A Sequence 12601, A Sequence 17063, A Sequence 17001, A Sequence 2094, App Sequence 4106, A Sequence 4106, A Sequence 17000, A Sequence 17, Appl Sequence 1703, Appl Sequence 1703, Appl Sequence 1703, Appl Sequence 1703, Appl Sequence 17103, Appl Sequence 24, Appl Sequence 17103, Appl Sequence 27, Appl Sequence 17103, Appl Sequence 27, Appl Sequence 17103, Appl Sequence 2813, A
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33.8	33.8	33.8	33.8	33.8	33.8	33.8	34	34	34	<b>34</b>	34.2	34.2	34.4	34.4	34.4	34.4	34.4	34.4	34.4	34.4
2.8	2.8	2.8			2.8		2.9	2.9	_	2.9	2.9	2.9		2.9		2.9				2.9
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US-09-949-016-15572	US-09-949-016-12655	US-09-780-049-18	US-09-949-016-17285	US-09-270-767-20152	US-09-270-767-4870	US-09-513-999C-32555	US-09-949-016-12448	US-09-949-016-17367	US-09-270-767-10251	US-09-270-767-25614	US-09-790-988-1	US-09-949-016-15698	US-09-949-016-13747	US-09-949-016-17422	PCT-US92-01385-3	US-08-245-809-4	US-08-107-748-3	US-09-845-849A-3	US-09-845-849A-1	US-09-060-726A-3
Sequence 15572, A	Sequence 12655, A	Sequence 18, Appl	Sequence 17285, A	Sequence 20152, A	Sequence 4870, Ap	Sequence 32555, A		Sequence 17367, A	Sequence 10251, A	Sequence 25614, A	Sequence 1, Appli	Sequence 15698, A	Sequence 13747, A	Sequence 17422, A	Sequence 3, Appli	Sequence 4, Appli	ω	ω	Sequence 1, Appli	Sequence 3, Appli

ALIGNMENTS

## RESULT 1 US-08-232-463-14/c Sequence 14, Application US/08232463 Patent No. 5670367 TELEX: 899149 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs GENERAL INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: STATE: V. STATE: VSA COUNTRY: USA COUNTRY: 2313-0299 NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEFAX: (703)683-4109 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/07/935,313 FILING DATE: APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: STREET: 1800 CITY: Alexandria CTATE: VA APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINANT NUMBER OF SEQUENCES: 52 IMMEDIATE SOURCE: CORRESPONDENCE ADDRESS: TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear APPLICATION NUMBER: FILING DATE: ADDRESSEE: pTZgpt-F1s E: Foley & Lardner 1800 Diagonal Road, US/08/232,463 Suite FOWLPOX VIRUS 500

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                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-41156
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US-09-949-016-41156
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 000-09-08
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                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRANCSEQ for Windows Version 4.0
SEQ ID NO 41156
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41156, Approximately Patent No. 6812339
                                                                                                                                                                                       Matches
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                       Match 3.1%;
Local Similarity 55.0%;
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                                                                        1070 ACCTATCAATGTTTTCTAGCTCCAAGCTAGCTATTGTTCATGTCCTAAGTTGCATGTGTA 1129
                                                                                                                                                  1011 TATCTTCGTCTAGATTTGTGTTATGTACTATTATCAGAGGGGTCTTGAATAT-TTGAAAA 1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               572 AATACATTAGAACCGATCCGCATATCTTAACGTATAAACCGGAATCTTTCGAGCTGGACA 631
                                                                                                                                                                                         94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRRRRRRRRRRRRRRRRATC 1064
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                                       AACTATCAATATTTTATTTTTCCTATCAAAAGATTGTATTTTTCTTATGTTTAGTTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTTTGTAGGTGGAATTGTGGGTTGCGTTTCTCAAGTATAGTTTGTGGGGTGAAAAAGCGG 931
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                                                                                                                                                                                       Conservative
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                                                                                                                                                                                   Score 37.4; DB 3;
Pred. No. 0.29;
0; Mismatches 76;
                                                                                                                                                                                       76; Indels
                                                                                                                                                                                                                        Length 601;
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PATENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-41157
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US-09-949-016-41157
                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12685, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 12685
LENGTH: 161900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 41157
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: CL001307
FEATURE: misc_feature NAME/KEY: misc_feature LOCATION: (1)...(161900) OTHER INFORMATION: n = A,T,C or
                                                                                              TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1070 ACCTATCAATGTTTTCTAGCTCCAAGCTAGCTATTGTTCATGTCCTAAGTTGCATGTGTA 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1011 TATCTTCGTCTAGATTTGTGTTATGTACTATTATCAGAGGGGTCTTGAATAT-TTGAAAA 1069
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                                                                                                                                                                                                            for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37.4; DB Pred. No. 0.29;
                                                                                                                                                                                                              4.0
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OF DETECTION AND USES THEREOF
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US-09-949-016-12906/c
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
    Sequence 12871, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 12906
LENGTH: 161914
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Best Local Similarity 55.0%;
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LOCATION: (1)...(161914)
OTHER INFORMATION: n = A
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les 94; Conserv
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J. Craig et al.
POLYMORPHISMS IN KNOWN GENES
WITH HUMAN DISEASE, METHODS
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  ASSOCIATED
OF DETECTION AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER: 07 SEQ ID NOS: 207012
SOFTWARE: FRASLSEQ for Windows Version 4.0
SEQ ID NO 12871
LENGTH: 100836
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ORGANISM: Human

PEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(100837)

OTHER INFORMATION: n = A,T,C

US-09-949-016-17063
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                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                   SEQ ID NO 17063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                        SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: CL001307
                                                                                                                                                    TYPE: DNA
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LOCATION: (1)...(100836)
OTHER INFORMATION: n = A,T,C
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Local Similarity 48.3%;
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Pred. No. 9.9;
0; Mismatches 109; Indels
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Best Local Similarity

3.1%;

Score 36.6; D Pred. No. 9.9;

BB

Length 100837;

Query Match

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RESULT 9
US-09-60-211A-2094
; Sequence 2094, Application US/09640211A
; Patent No. 6833446
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, NAME/KEY: misc feature
; LOCATION: (1)...(317366)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-16001
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US-09-949-016-16001
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LENGTH: 317366
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR TILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREUSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
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                                                                                                                         ATGGGGTTTT
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                                                                                                                                                                                                    ACTITIATITIAGGITCAGGGGTACATGTGCAGGTTTGTTATATAGGTATACTTCATGTC 151834
                                                                                                                                                                                                                                         AGCTATTGTTCATGTCCTAAGTTGCATGTGTATTTTATTAAACTCGATCAAAACATTTG 1157
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Pred. No. 22;
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APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.102101U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2094
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SOPTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 354, Application US/09640211A Patent No. 6833446
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APPLICANT: Shenk, Micha
APPLICANT: McGrath, An
APPLICANT: Glenn, Matt
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TYPE: DNA
ORGANISM: Pinus radiata
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TYPE: DNA
ORGANISM: Pinus radiata
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Local Similarity 51.2%;
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                                                                                                                                           619 TTCGAGCTGGACATACCGGTTGCAGTGGTGGGAACCGGACTCGGACCGAAGTGGAACAAC
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McGrath, Annette
Glenn, Matthew
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                         GAGCTGGCATCATGTGCATTGAAGGATTTGAATCAGTTGGAG
                                                                                                      GAAGGAAGTGACACGAGTACATCAAAAGAGCAAGATGTCCAGTGTTTAAAACGAGAAAGT
                                                            GTGATGCCACCATGCGCACCAACGGACTTAAACCATGAGGAG
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51.2%;
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US-09-710-279-4106/c
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; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4106
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US-09-949-016-17000/c
                                                                                 Query Match
Best Local S
Matches 91
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERWIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4106
LENGTH: 3769
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Patent No. 6703492
GENERAL INFORMATION:
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LENGTH: 57638
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
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SOPTWARE: FASTSEQ for Windows Version
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LOCATION: (1)...(57638)
OTHER INFORMATION: n = A,T,C
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ORGANISM: Human
                                                                                 Local Similarity
nes 91; Conserv
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                                      AAGCTTCTGGTATCTTCGTCTAGATTTGTGTTATGTACTATTATCAGAGGGGGTCTTGAAT 1060
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Pred. No. 4.2;
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Pred. No. 17;
0; Mismatches
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                                                                                                                      Length 3769;
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US-09-949-016-13353
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US-09-710-279-4133/c
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION ITLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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Patent No. 6703492
GENERAL INFORMATION:
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Patent No. 6812339
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Best Local Similarity
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CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC
FILE REFERENCE: PU3480US
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Pred. No. 4.5;
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; PRIOR APPLICATION NUMBER: 60/231,498; PRIOR FILING DATE: 2000-09-08; NUMBER OF SEQ ID NOS: 207012; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 13353; LENGTH: 124110; TYPE: DNA; ORGANISM: Human; ORGANISM: Human
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US-08-222-719-17
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US-08-222-719-17
                                                TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 862
TYPE: nucleic acid
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Patent No. 5846711
GENERAL INFORMATION:
APPLICANT: David D. Moore
APPLICANT: Jae Woon Lee
TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-
TITLE OF INVENTION: INTERACTING POLYPEPTIDES AND
TITLE OF INVENTION: RELATED MOLECULES AND METHODS
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WORDER: US/08/222,719
FILING DATE: WORDER: US/08/222,719
FILING DATE: 04-April-1994
CLASSIFICATION DATA:
APPLICATION UNMBER: US/08/22,719
FILING DATE: 04-April-1994
CLASSIFICATION DATA:
APPLICATION UNMBER: 07/969,136
FILING DATE: 30-October-1992
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 00786/229001
TELEPANCE/DOCKET NUMBER: 00786/229001
TELEPONE: (617) 542-8906
TELEPAN: 20154
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                  STRANDEDNESS: don TOPOLOGY: linear
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STATE: Massac
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Search completed: March 20, 2006, 14:05:53 Job time : 240.782 secs
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Best Local Similarity 64.2%;
Matches 52; Conservative
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Pred. No. 2.8;
0; Mismatches 29;
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AP004274 Oryza sat E63080 DNA encodin	Continuation (281	BT009115 Triticum	AX411615 Sequence	BT008923 Triticum	AX411625 Sequence	AF134301 Chenopodi	AB025025 Chenopodi	E63070 DNA encodin	AE017095 Oryza sat	AC027658 Oryza sat					AB056126 Citrus un			AX411609 Sequence	BT009214 Triticum	AX411617 Sequenc	AX411607 Sequence	AY099815 Arabidops	AF021244 Arabidops	E63071 DNA encodin	BT000309 Arabidops

## ALIGNMENTS

RESULT 1
E33072
E33072
B63072
B73072

Query Match 100.0%; Score 1135; DB 6; Length 1135; Best Local Similarity 100.0%; Pred. No. 5.7e-271; Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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                                                                                                                     GTTCCCGTTGAAATTCAAGAGTTTGAGGTTATCATGTAAACATAAGTTTTTCTTTAGGGG
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Cloning of chlorophyllase, the key enzyme in chlorophyll degradation: finding of a lipase motif and the induction
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LLVATPVEEGDYPVVMLHFLFAQVTPMLSKFALSGHSRCGKTAFAVALKKFGYSSNILKI
STLIGIDPVDGTGKGKQTPPPVLAYLFNSFDLDKTPILVIGSGLGETARNPLFPPCAP
PGVNHREFFREQQGFAMHFVAKDYGHLDMLDDDTKGIIGKKSSYCLCKNGEERREMRRF
VGGLVVSFLKAYLEGDDRELVKIKDGCHEDVPVEIQEFEVIM"
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/EC_number="3.1.1.14"
/note="chlorophyllase 2; hydrolase; includemotif and lipase/serine active site motif"
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/mol_type="mRNA"
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                                                                 GI:27754533
                                                                                                   linear
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Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.
Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C.,
Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,
Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M.,
Southwick, A., Tripp, M.G., Wu, T., Satou, M., Seki, M., Shinn, P.,
Ecker, J.R. and Theologis, A.
Arabidopsis Full Length cDNA Clones
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Street, Albany, CA 94710, USA RIXEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIXEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida, Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Annotation based on July 2002 version submitted to Genbank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
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                                                   /gene="At5g43860"
note="compared to genomic acid sequence difference"
                                                                                                                                                                                                                   /translation="SCCCKITPSSRASPSPPKQLLVATPVEEGDYAVVMLLHGYLLYNSFYSQLMLHYSHGFILIAPQLYSIAGEDTWDEIKSTAEIMMHSVGLMHFLPAQVTPNLSKFALSGHSHGSKGTPPPVLAYLLSKEALSGHSHGSKGKGTPPVLAYLLSKEALSGHSHGSKGKGTPPVLAYLLSKEALSGHSHGSKGKGTPARVLFFPPCAPGVMHEFFRECQGFAKHFVAKDYGHLMLDDDTKGIRGKSSYCLCKNGEERRPMRRFVGGLVVSFLKAYLEGDDRELVKIKDHLDDDTKGIRGKSSYCLCKNGEERRPMRRFVGGLVVSFLKAYLEGDDRELVKIKD
                                                                                                                                                                                      HLDMLDDDTKGIRGKSSYCLCKNGEERRPMRRFVGGLVVSFLKAYLEGDDRELVKI.
GCHEDVPVEIQEFEVIM"
                                                                                                                                                                                                                                                                                                                                                                   /evidence=experimental
/product="putative AtCLH2
/protein_id="AAO22714.1"
/db_xref="GI:27754534"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="This clone is in a modified (lambda PS) as a BamHI/XhoI insert.
                                replace="c"
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/ecotype="Columbia"
/note="This clone is in
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/chromosome="5"
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                                                                                                                                     GGACATGCTTGATGATGATACAAAAGGGATTAGAGGGAAGAGTTCTTATTGTTGTGTAA 836
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GGATGTTCCCGTTGAAATTCAAGAGTTTGAGGTTATCATGTAAACATAAGTTTTTCTTTA
                                              GAAGGCTTATTTGGAAGGAGATGATCGTGAATTAGTTAAGATCAAAGATGGGTGTCACGA
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                                                                                                                                                                                                                                                                                                                                                                Address for correspondence: Kaos@kazusa.or.jp
Address for correspondence: Kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MQD19
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://cCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebbsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).

This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
Thosation/Oualifiers

The 5' clone is MQO24 and the 3' clone is F686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1077
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (28-APR-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mailynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Tabata,S,
Structural analysis of Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB026651 BA000015
AB026651.1 GI:4757407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko, T., Katoh, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 87286)
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                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                               2159
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me 5, Pl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(12391. .12699,12792. .12855,12945. .13059, 13177. .13315,13415. .13542,13630. .13759,13977. .14129))
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CDS

Sg

gg

Query Match Best Local Sim Matches 806;

Similarity

70.7%;

Pred. 0; Mi Score 803;

Mismatches

ŏ.

1.5e-188; ches 5; DB 15;

Indels

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Gaps

0

Conservative

Sd

SgS

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                                                                       evidence=not_experimental
                                                                                                                                           join(40794. .41579,42574. .43377)
/note="gene_id:MQD19.11"
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/db_xref="GI:10177943"
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Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (Dases 1 to 1104)

Chen, H.-H., Chou, Y.-F. and Shaw, J.-F.

Molecular characterization and differential regulation of three chlorophyllase genes, members of the novel serine esterase gene
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Brassica oleracea chlorophyllase
AF337545 GI:24210534
                                                                                                                                           Brassica oleracea
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Unpublished
2 (bases 1 to 1104)
2 (hases 1 to 104)
Chen,H.-H., Chou,Y.-F. and Shaw,J.-F
Direct Submission
Submitted (18-JAN-2001) Institute of
Taipei, Taiwan 11529, Republic of Ch
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/product="chlorophyllase 2"
/protein_id="AAN51934.1"
/db_xref="GI:24210535"
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LKISALIGVDFVDGTGKGKOTPPVLTYENSFNLEMPVLVISGLGELARNPLFPP
CAPTGVNHREEFOECGPAWHFVAKUYGHLDWLDDDTKGLRGKSYCLCKNGEERKPM
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REFIGGIVSFLMAYLEDDDCELVKIKAGCHEGVPVEIQEFEVKK"
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/mol type="mRNN"
/culfivar="Green king"
/db_xref="taxon:3712"
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Pred. No. 4.9e-174;
0; Mismatches 170;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermarophyta; Magnoliophyta; Enassicaceae; Brassica.
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Chen, H.-H., Chou, Y.-F. and Shaw, J.-F.
Molecular characterization and differential regulation of three chlorophyllase genes, members of the novel serine esterase gene
                                                                                                                                                                       Submitted (18-JAN-2001) Institute of Botany, Taipei, Taiwan 11529, Republic of China
                                                                                                                                                                                              Chen, H.-H., Chou, Y.-F. and Direct Submission
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/culfivar="Green king"
/db_xref="taxon:3712"
                                               note="BoCLH3"
                                                          EC_number="3.1.1.14"
                                                                                         tissue_type="floret"
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AX411603
Sequence 3
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Vitis sp.
Vitis sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Vindiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
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PONT DE NEMOURS AND COMPANY
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                                                                                                            Location/Qualifiers
                                            organism="Vitis sp."
/mol_type="unassigned
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-MAY-2004) The Institute for Genomic Medical Center Drive, Rockville, MD 20850, USA Location/Qualifiers
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FLI_CDNA.
Lycopersicon esculentum
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Kirkness, E.F., Wang, W. and Vazeille,
Direct Submission
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                TCTTATTGTTTGTGTAAGAATGGTGAAGAGAGAGAGACCAATGAGGAGATTCGTTGGTGGA
                                                                        AAGGATTATGGGCATTTGGACATGCTTGATGATGATACAAAAGGGATTAGAGGGAAGAGT
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Gaps

	COMMENT	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	RESULT 9 APO07972 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	00 QV 90 90 90 90 90 90 90 90 90 90 90 90 90
* be preserved.  1715 contig of 1715 bp in length 1816 2641: contig of 826 bp in length 2642 2741: gap of unknown length 2742 3555: contig of 836 bp in length 3556 4548: contig of 814 bp in length 3556 4548: contig of 893 bp in length 4649 6180: contig of 1532 bp in length 6181 7099: contig of 1532 bp in length 7100 7199: gap of unknown length 840 9486: contig of 1810 bp in length 940 9486: contig of 1100 bp in length 940 9486: contig of 1047 bp in length 11122 11221: gap of unknown length 11122 1221: gap of unknown length 1122 12794: contig of 1535 bp in length 11385 14686: contig of 1579 bp in length 11487 16382: contig of 1792 bp in length	RL:h ax:8 NOT con is arb run Thi	Kaneko,T., Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S. Kaneko,T., Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S. Structural Analysis of a Lotus japonicus Genome. XI. Sequence Features and Mapping of Nine hundred twenty-one TAC Clones Unpublished (bases 1 to 128855) (bases 1 to 128855) Sato,S. Direct Submission Submitted (26-OCT-2004) Shusei Sato, Kazusa DNA Research Institute, Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan (E-mail:ssato@kazusa.or.jp,	AP007972  128855 bp DNA linear HTG 28-DEC-2004 LOTUS COTNICULATUS VAR. japonicus chromosome 5 clone LjT44A18, *** SEQUENCING IN PROGRESS ***, 45 unordered pieces. AP007972.1 GI:56806280 HTG, HTGS, PHASE1. LOTUS COTNICULATUS VAR. japonicus (Lotus japonicus) LOTUS COTNICULATUS VAR. japonicus (Lotus japonicus) ENKATYOLE, VIridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Pabaceae; Papilionoideae; Loteae; Lotus	880 CTTGTTGTATCATTTTTGAAGGCTTATTTGGAAGAGAAGATGATCGTGAAATTAGTTAAGATC 939
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79116 83509 83609 87606 87706 92816 92816 92817 102877 102877 108288 108388 112791 1127974 127874 127974 12	62615 62715 65636 65636 65841 69841 73813 73913	599822224	29433 31533 31533 31633 31633 36056 36056 36056 36056 36056 36056	1648 1784 194 1913 1923 1923 1923 1923 1923 1923 1923
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Score 281.6; DB 14;
Pred. No. 5.8e-59;
       Length 128855;
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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                RESULT 10
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Sequence
AX411613
                                                                                                                         fulipa.
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Tulipa gesneriana
Tulipa gesneriana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
                                                                                    Chlorophyllases
Patent: WO 0229022-A 13 11-APR-2002;
E.I. DU PONT DE NEMOURS AND COMPANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 AX411613.1
                                                                                                                                                                           Thorpe, C.,
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/organism="Tulipa gesneriana"
/mol_type="unassigned DNA"
/db_xref="taxon:13306"
                                                                                                                                                                       Cahoon, E.B.
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                FEATURES
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Ginkgo biloba
AY292526
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                                                          Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Ginkgophyta; Ginkgoales; 1 (bases 1 to 1157)
Okazawa, A., Tang, L., Fukusaki, E.-I. and Direct Submission
                                                                                                                                          Ginkgo biloba (maidenhair tree)
Ginkgo biloba
 Submitted (06-MAY-2003) Department University, 2-1, Yamadaoka, Suita, Docation/Qualifiers
1. .1157
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                                                                                                         Embryophyta;
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                     TTCGTTGCGAAGGATTATGGGCATTTGGACATGCTTGATGATGATACAAAAGGGATTAGA
                                                                                                                                            GCACCTCCCGGAGTGAATCACCGAGAGTTCTTTCGGGAATGTCAAGGTCCAGCATGGCAT
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                                                          TITGTTGCCTCTGATTATGGGCATCTTGATTTCTTAGACGACGACACCAAAGGAATAAGA
                                                                                                                         GCTCCCCAAGGTGTTAACCACCATGATTTCTTCTACGAATGTGTCGCTCCTGCCTATCAT
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55. .1083
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/mol_type="mRNA"
/db_xref="taxon:3311"
1. ..1157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAP44978.1"
/db_xref="GI:31415500"
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/product="chlorophyllase"
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Pred. No. 2.3e-50;
0; Mismatches 301;
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                           TGATCGGTTCGGGGCTTGGTGAAACCGCTCGGAACCCATTATTCCCACCGTGTGCACCTC
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TAATCGGCACGGGTTGGGCGATGAGCCAAGGAACTGCCTAACATGTCCATGTGCCCCAG
                                                                        TTCCCAAAATCCTAACCTATGTTCCTCATTCCTTCAATCTAG---CAATCCCAGTTTGCG
                                                                                                    CTCCTCCGGTGTTGGCTTACCTTCCAAACTCATTTGACCTAGACAAAACGCCTATACTTG
                                                                                                                                                 ACTTCTCAGCCCTACTAGGACTAGACCCTGTTGGTGGGTTGAGTAAATGTTGCCAAACAG
                                                                                                                                                                                    GAGGGGAAAGACAGCATTTGCTCTGGCACTAGGGTATGCTGATACATCC
                                                                                                                                                                                                                                                             GCGGTGGCAAAACCGCGTTTGCGGTCGCCTTAAAGAAATTTGGGGTACTCCTCGAATCTAA
                                                                                                                                                                                                                                                                                                      CTGTGCTCCCAGAAAATGTGAAACCAGACCTACTCAAGCTTGCTCTTTCAGGCCACAGCA
                                                                                                                                                                                                                                                                                                                                          ACTITCTTCCAGCGCAAGTAACACCAAACCTATCCAAATTTGCCCTCTCCGGCCATAGCC
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PONT DE NEMOURS AND COMPANY
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/mol_type="unassigned
/db_xref="taxon:3604"
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Pred. No. 7.1e-48;
0; Mismatches 411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                            PUBMED
                           Direct Submission

Direct Submission

Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment(s) resulting from

the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding mutant line and a link to a database providing a

graphical display of the insertion site are available at

http://dbsgap.versailles.inra.fr/publiclines/. This sequence has

been generated in the framework of the French plant genomics

program 'Genoplante' (http://www.genoplante.com and

http://genoplante-info.infobiogen.fr).
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Balzergue, S.
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T-DNA integration into the Arabidopsis genome depends on sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunaud, V.,
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Left border; T-DNA flanking sequence
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Sequence 5 :
AX411605
AX411605.1
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Patent: WO 0229022-A 5 11-APR-2002;
E.I. DU PONT DE NEMOURS AND COMPANY
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mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                     GAGATTATCCGGTGGTGATGCTCCATGGTTACCTTCTACAACTCCTTCTATTCTC 262
TCGCCGGACCAGACACAATGGATGAGATTAAATCAACGGCGGAGATTATGGATTGGTTAT 382
                                  AGCTTATGTTGCATGTCTCTCTCATGGCTTCATCCTCATCGCTCCTCAGTTATATAGTA 322
                                                                 GGGAGTACCCGGTGATCCTGTTCCTACACGGCTACCTCGCCGTCAACTCCTTCTACTCCC 360
                                                                                                                CTTCTAGAGCTTCACCGTCTCCGCCAAAGCAGCTGTTGGTGGCTACGCCGGTGGAGGAAG
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                     AGCTGTTCGAGCACGTCGCCTCCCATGGCTTATCGTCGGCACCTCAGCTGTACACCA
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                                                                                                                                                                                                                    /organism="Zea mays"
/mol_type="unassigned
/db_xref="taxon:4577"
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|mol type="genomic DNA"
|db xref="taxon: 3702"
|clone="076H05"
|clone lib="Arabidopsis thaliana
|ecotype="Wassilewskija"
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left border"
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Pred. No. 5.5e-39;
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Pred. No. 6.4e-44;
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j. .1115

/organism="Brassica oleracea"

of Botany, China

Academia

/mol\_type="mRNA" /cultivar="Green king" /db\_xref="taxon:3712"

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Direct Submission
Submitted (18-JAN-2001) Institute
Taipei, Taiwan 11529, Republic of
Location/Qualifiers
                                                                                                                                                                  1 (bases 1 to 1115)
Chen, H. -H., Chou, Y. -F. and Shaw, J. -F.
Molecular characterization and differential regulation of three chlorophyllase genes, members of the novel serine esterase gene
                                                                                   2 (bases 1 to 1115)
Chen, H.-H., Chou, Y.-F.
                                                                                                                                                                                                                                                                                                                  Brassica oleracea
Brassica oleracea
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                           AGACCAATGAGGAGATTCGTTGGTGGACTTGTTGTATCATTTTTGAAGGCTTATTTGGAA
                                                                                         TTGCCCGGTTTTGTCGGGTTTATGGCGGGTTGTATGTGTAAGAACGGTAAACGCAAAAAG
                                                                                                                            ACAAAAGGGATTAGAGGGAAGAGTTCTTATTGTTTTGTGTAAGAATGGTGAA----GAGAGG
                                                                                                                                                                                          GCTACGAAGGGACATTTCGTGGCTGCGGATTACGGACATATGGATATGTTGGACGATAAT
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FSALVGIDPVAGISKCIATDPBILTTYKPESFDLDMFVAVIGTGLGFKSMUKMFCAPA
EVNHEEFYIECKATKGHFVAADYGHMDMLDDNLPGFVGFMAGCMCKNGKRKKSEMRSF
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Search completed: March Job time : 4016.27 secs 20, 2006, 16:11:53

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
         622.2
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13.2	13.6	13.6	14.3	14.5	14.9	15.2	15.4	15.7	16.0	16.2	16.2	16.7	16.8	17.1	17.2	17.3	17.5	18.1	18.1	18.2	18.8	19.4
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ALIGNMENTS

## DOURNAL TITLE Large scale analysis of Arabidopsis full-length cDNA TITLE JOURNAL COMMENT Tell scales for the scales of the scale

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                                      Mathur, J., Szabados, L., Schaefer, S., Grunenberg, B., Lossow, A., Jonas-Straube, E., Schell, J., Konzz, C. and Konzz-Kalman, Z. Gene identification with sequenced T-DNA tags generated by transformation of Arabidopsis cell suspension Plant J. 13 (5), 707-716 (1998)
                                                                                                                                                                                                                                                     AF005802 Arabidopsis thaliana 188-4 Arabidopsis thaliana genomic clone 1884xa similar to EST with GenBank Accession Number R30366,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 CAGTTATATAGTATCGCCGGACCAGACACAATGGATGAGATTAAATCAACGGCGGAGATT
                                                                                                                         790
                                                                                                                                                                                                         730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Max-Planck Institut fuer Zuechtungsforschung Carl von Linne weg 10, Cologne, D-50829, Germany Email: konczempiz-koeln.mgg.de transgenic cell line was obtained by transformation with the T-DNA of pPCV6NFHyg Agrobacterium binary vector; the left border junction of T-DNA insertion 1884xa was isolated in E. coll after XbaI digestion and self-circularization of plant DNA; clone 1884xa carries a plant DNA fragment of 5.0 kb that extends from a XbaI site to the left-border junction of pPCV6NFHyg T-DNA tag; sequences of the left T-DNA border are excluded from the submission class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGATTGGTTATCAGTAGGACTTAATCACTTTCTTCCAGCGCAAGTAACACCAAACCTA 429
                                     AGGAGACCAATGA 862
                                                                             AACCCATTATTCCCACCGTGTGCACCTCCCGGAGTGAATCACCGAGAGTTCTTTCGGGAA
                                                                                                                                                                                                                                                                                                                                                              TTTGACCTAGACAAAACGCCTATACTTGTGATCGGTTCGGGGCCTTGGTGAAACCGCCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                         GATGGAACAGGGAAAAGGGAAACCCCCTCCTCCGGTGTTGGCTTACCTTCCAAACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGGAACAGGGAAAGGGAAACAAACCCCTCCTCCGGTGTTGGCTTACCTTCCAAACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGAAATTTGGGTACTCCTCGAATCTAAAGATCTCGACATTGATCGGTATAGATCCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGAAATTTGGGTACTCCTCGAATCTAAAGATCTCGACATTGATCGGTATAGATCCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCAAATTTGCCCTCTCCGGCCATAGCCGCGGGGGCAAAACCGCGTTTGCGGTCGCCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGTTATATAGTATCGCCGGACCAGACACAATGGATGAGATTAAATCAACGGCGGAGATT
                                                                                                                                                                                                         TGTCAAGGTCCAGCATGGCATTTCGTTGCGAAGGATTATGGGCATTTGGACATGCTTGAT 789
                                                                                                                                                                                                                                                     AACCCATTATTCCCACCGTGTGCACCTCCCGGAGTGAATCACCGAGAGTTCTTTCGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCAAATTTGCCCTCTCCGGCCATAGCCGCGGTGGCAAAACCGCGTTTGCGGTCGCCTTA
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                                                                                                                                                                                                                                                                                                                                       TTTGACCTAGACAAAACGCCTATACTTGTGATCGGTTCGGGGGCTTGGTGAAACCGCTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_line="188-4"
/clone_lib="Arahia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis
/mol_type="genomic DNA"
/ecotype="Col-1"
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/clone="1884xa"
/cell_line="188-4"
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Pred. No. 4.3e-125;
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GSS 06-NOV-2000

genomic

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GSS 01-APR-2004

genomic

clone

Cotton, D.,

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Patton, D.,

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FEATURES
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Abtellung Genetische Grundlagen der Pflanzenzuechtung
Max-Planck Institut fuer Zuechtungsforschung
Carl von Linne weg 10, Cologne, D-50829, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: koncz@mpiz-koein.mpg.de

T-DNA tagged line 031-2, PCR fragment 031-2XA; Transgenic plant
line 031-2 was obtained by transformation with the T-DNA of
pPCV6NFHyg Agrobacterium binary vector; the left border junction of
T-DNA insertion 031-2XA was isolated by PCR amplification using the
LB2 (5'-CTGGGGAATGCGGAATCAAGGCATCGATCGGAAG-3') and PC3

(5'-CCTTGCGCCTGAGTGCTTGCGGCAGC-3') primers and sequenced with the
PC3 primer as described by Mathur et al. Plant J. (1998) 13,
707-716; the PCR-amplified DNA fragment extends from an XbaI site
to the left border junction of pPCV6NFHyg T- DNA tag, sequences of
the left T-DNA end are excluded from the submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koncz,C., Szabados,L., Gruneberg,B. and Schaefer,S. Gene identification with sequenced T-DNA tags in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1998)
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                          TGTCAAGGTCCAGCATGGCATTTCGTTGCGAAGGATTATGGGCATTTGGACATGCTTGAT 789
                                                                                                                                                                TITGACCTAGACAAAACGCCTATACTTGTGATCGGTTCGGGGGCTTGGTGAAACCGCTCGG 459
                                                                                                                                                                                                                                                  GATGGAACAGGGAAAGGGAAACAAACCCCTCCTCCGGTGTTGGCTTACCTTCCAAACTCA
                                                                                                                                                                                                                                                                                         GATGGAACAGGGAAAGGGAAACAAACCCCCTCCTCCGGTGTTGGCTTACCTTCCAAACTCA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGATTGGTTATCAGTAGGACTTAATCACTTTCCTTCCAGCGCAAGTAACACCAAACCTA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGTTATATAGTATCGCCGGACCAGACACAATGGATGAGATTAAATCAACGGCGGAGATT 369
                                                                                                         AACCCATTATTCCCACCGTGTGCACCTCCCGGAGTGAATCACCGAGAGTTCTTTCGGGAA 729
                                                                                                                                                                                               TTTGACCTAGACAAAACGCCTATACTTGTGATCGGTTCGGGGGCTTGGTGAAAACCGCTCGG
                                                                                                                                                                                                                                                                                                                                                                                  AAGAAATTTGGGTACTCCTCGAATCTAAAGATCTCGACATTGATCGGTATAGATCCAGTC 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCAAATTTGCCCTCTCCGGCCATAGCCGCGTGGCAAAACCGCGTTTGCGGTCGCCTTA 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGGATTGGTTATCAGTAGGACTTAATCACTTTCTTCCAGCGCAAGTAACACCAAACCTA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGTTATATAGTATCGCCGGACCAGACACAATGGATGAGATTAAATCAACGGCGGAGATT 159
TGTCAAGGTCCAGCATGGCATTTCGTTGCGAAGGATTATGGGCATTTGGACATGCTTGAT 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 624)
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llarity 100.0%;
Conservative
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="CO1-0"
/db_xref="taxon:3702"
/clone="031-2XA.PC3"
/clone_lib="Arabidopsis thaliana C
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Pred. No. 1.5e-121;
0; Mismatches 0;
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JOURNAL
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Best Local Similarity
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                                                                                                                                                                                                                                                                                              411 GCAAGTAACACCAAACCTATCCAAATTTGCCCTCTCCGGCCATAGCCGCGGTGGCAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: allen.sessions@syngenta.com
ABRC Stock Number CS827897; T-DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and not single contiguous sequences.

Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patl Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J.D., Cotton, Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B., Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S.A. A high-throughput Arabidopsis reverse genetics system Plant Cell 14 (12), 2985-2994 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; coreosids II; Brassicales; Brassicaceae; Arabidopsis.
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                      GGCTTACCTTCCAAACTCATTTGACCTAGACAAAACGCCTATACTTGTGATCGGTTCGGG
                                                                                                           GCAAGTGGCCACAAACCTATCCAAATTTGCCCTCTCCGGCCATACCCGCGGTGGCAAAGC
                                                                                                                                                                                                                                                                                                                                                                TAAATCAACGGCGGAGATTATGGATTGGTTATCAGTAGGACTTAATCACTTTCTTCCAGC
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GGCTTACCTTCCAAACTCATTTGACCTAGACAAAACGCCTATACTTGTGATCGGTTCGGG
                                                                                                                                                                CGCGTTTGCGGTCGCCTTAAAGAAATTTGGGTACTCCTCGAATCTAAAGATCTCGACATT
                                                                                                                                                                                                        CGCGTTTGCGGTCGCCTTAAAGAAATTTGGGTACTCCTCGAATCTAAAGATCTCGACATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="SAIL 646_E09.v1"
/clone_1ib="SAIL Collection"
/note="T-DNA left border sequences
modified TAIL-PCR strategy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         44.78;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 507.8;
Pred. No. 3.6e
0; Mismatches
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Arabidopsis thaliana
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3.6e-117;
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Indels Length

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470 552

372 650 432 590 492 530 were

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AUTHORS
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BP789041 RAFL7 Arabidopsis th
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified pBluescript vector.
Please visit our web site (http://pfgweb.gsc.riken.jp and http://rarge.gsc.riken.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN Genomic Sciences Center
3-1-1 Koyada1, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Pax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seki,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Iida,K., Enju,A., Sakurai,T., Arakawa,T., Carninci,P., Fukuda,S., Iida,J., Kawai,J., Sasaki,D., Shiraki,T., Hayashizaki,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998, 2002).This clone is in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Motoaki Seki
Plant Functional Genomics Research Group
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Unpublished (2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCATTTGGACATGCTTGATGATGATACAAAAGGGATTAGAGGGAAGAGTTCTTATTGTTT
CAAGGTCCAGCATGGCATTTCGTTGCGAAGGATTATGGGCATTTGGACATGCTTGATGAT
                                                                                CCATTATTCCCACCGTGTGCACCTCCCGGAGTGAATCACCGAGAGTTCTTTCGGGAATGT 732
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                                                             CCATTATTCCCACCGTGTGCACCTCCCGGAGTGAATCACCGAGAGTTCTTTCGGGAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGAGAGTTCTTTCGGGAATGTCAAGGTCCAGCATGGCATTTCGTTGCGAAGGATTATGG
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                                                                                                                                    35.2%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                 /note="Site 1: BamHI; Site 2: SalI; subjected
cold-treated (1, 2, 5, 10, 24 hr)"
                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                          /dev_stage="rosette plants"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                  clone_lib="RAFL7"
                                                                                                                                                                                                                                                                                                                               clone="RAFL07-36-K05"
                                                                                                                                                                                                                                                                                                                                                                                 organism="Arabidopsis"
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                                                                                                                                    Score 399; DB 3;
Pred. No. 1e-89;
0; Mismatches 0
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  Query Match 35.1%;
Best Local Similarity 98.8%;
Matches 401; Conservative
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Contact: Motoaki Seki
                                                                                                                                                                                                                                                                                                                                                        Bmail: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: 81-328-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL15-48-F08"
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                        /tissue_type="mixture of
/lab_host="DH10B"
                                                                                                     clone_lib="RAFL15"
note="Site_1: BamHI; Site_2:
                                                                                                                                                                                                                                                                    organism="Arabidopsis"
                                                                                                                                   lib="RAFL15"
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Score 398; DB 1; -
Pred. No. 1.8e-89;
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                                              DB 1; Length 413;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP786753 RAFL7 mRNA sequence.
                                                                                                                                                                                           Email: msekl@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998, 2002). This clone is in a
modified pBluescript vector.
Please visit our web site (http://pfgweb.gsc.riken.jp and
http://rarge.gsc.riken.jp) for further details.
                                                                                                                                                                                                                                                                                                                      Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seki, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K., Iida, K., Enju, A., Sakurai, T., Arakawa, T., Carninci, P., Fukuda, S., Iida, J., Kawai, J., Sasaki, D., Shiraki, T., Hayashizaki, Y. and
                                                                                                                                                                                                                                                                                                          Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                       Large-Scale Analysis of RIKEN Arabidopsis Full-length cDNAs Unpublished (2005)
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Arabidopsis thaliana
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BP786753.1 GI:59263657
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                                                /mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFLZ6-01-124"
/dev_stage="rosette plants"
/lab_host="DH10B"
      /clone_lib="RAFL7"
/note="Site_1: BamHI; Site_2:
cold-treated (1, 2, 5, 10, 24
                                                                                                                       organism="Arabidopsis/mol_type="mRNA"
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                                                                                                                                                                                                                                    Beijing AgroBiotechnology Research Center
Haidian District, Ban-Jing Rd., Beijing 100089, China
Tel: 86 10 5150 3881
Fax: 86 10 5150 3980
                                                                                                                                                                                                                                                                                                   Contact: Rongcai, Ma
Plant Functional Genomics
                                                                                                                                                                                                                                                                                                                                     Gao,R.J., Dai,D.P. and M
Expressed sequence tags
of Chinese cabbage
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                    Email: rcmal@yahoo.com
Seq primer: T7
High quality sequence stop:
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CA992230.1 GI:37621525
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/organism="Brassica rapa subsp. pv
/mol type="mRNA"
/sub species="pekinensis"
/db_xref="taxon:51351"
/tissue type="heading leaf"
/dev_stage="folding stage"
/lab_host="E.coli DHIOB(ZIP)"
/clone_lib="GIBCOBRL CAT. NO. 196.
                                                                                                                                                      Location/Qualifiers
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HC0819 GI
                                                                          Plant Functional Genomics
Beijing AgroBiotechnology Research Center
Haidian District, Ban-Jing Rd., Beijing 10
Tel: 86 10 5150 3980
Email: rcmal@yahoo.com
                                                                                                                                                                    Gao,R.J., Dai,D.P. and Ma,R.C. Expressed sequence tags of heading of Chinese cabbage Unpublished (2003)
                                                                                                                                                                                                                                    Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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CA992233
CA992233.1 GI:37621528
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                                                                                                                                                        Contact: Rongcai, Ma
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                                                  quality sequence
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                        Location/Qualifiers
/organism="Brassica rapa
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Pred. No. 1e-7:
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CX076457.1
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Contact: Timothy J. Close
Department of Botany & Plant
University of California
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UCRCS08_50B04_g I
UCRCS08-2 Citrus
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Pred. No. 3.4
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S 문 ક 닭 र् 밁 ð 밁 Ś 밁 ð 밁

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/mol type="mRNA"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/db_xref="taxon:51351"
/tissue_type="heading leaf"
/tissue_type="heading leaf"
/dev_stage="folding stage"
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/clone_lib="GIBCOBRL CAT. NO. 19643-014"
/note="Vector: pZL1; Site_1: Not1; Site_2: Sal1; cDNA
/note="Vector: pZL1; Site_3: SITE Z: Sal1; cDNA
library was constructed by SUPERSCRIPTTM Lambda System f
cDNA Synthesis and Cloning (GIBCOBRL, CAT.NO.19643-014)"
                                                              for
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GAAACAAACCCCTCCTCCGGTGTTGGCTTACCTTCCAAACTCATTTGACCTAGACAAAAC ATTAGTTAAGATCAAAGATGGGTGTCACGAGGATGTTCCCGTTGAAATTCAA GCATTTTGTCGCAAAGGATTACGGACATTTAGACATGCTTGATGATGATACAAAAGGGCT GCATTTCGTTGCGAAGGATTATGGGCATTTGGACATGCTTGATGATGATACAAAAGGGAT GTGTGCACCTACGGGAGTGAACCACCGAGAGTTTTTCCAGGAATGTCAAGGTCCAGCGTG TCGAATCTAAAGATCTCGACATTGATCGG-TATAGATCCAGTCGATGGAACAGGGAAAGG GTGTGCACCTCCCGGAGTGAATCACCGAGAGTTCTTTCGGGAATGTCAAGGTCCAGCATG GCCTGTTCTAGTTATTGGTTCGGGACTTGGTGAACTTGCCCGGAACCCATTGTTTCCACC GCCTATACTTGTGATCGGTTCGGGGCTTGGTGAAACCGCTCGGAACCCATTATTCCCACC TAAACAAGCCCCTCCTCCGGTTTTAACCTATGAACCAAACTCATTTAACCTAGAAAAGAT GTTGATGAAGATCAAAAATGGGTGTCATGAAAGTGGTCCTGTTGAAATTCAA ATTTATTGGTGGTATTGTTGTGTCGTTTTTGATGGCTTATCTGGAAGATGATGATTGTGA TAGAGGGAAGAGTTCTTATTGTTTGTGTAAGAATGGTGAAGAGAGAAAACCAATGAGGAG TCGGAACTAAAGATCTCAGCACTTATCGGTTGTAGATCCGGTGGATGGGACAGGGAAAGG 1.4e-75; 1es 74; 밁 6, Indels Length 494; 1; Gaps 361 301 241 181 686 121 61 421

Citrus sinensis
Citrus sinensis
Citrus sinensis
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids, eurosids II; Sapindales; Rutaceae; Citrus. 1 (bases 1 to 749)
Close, T.J., Roose, M.L., Ye, X.R., Fenton, R.D., Wanamaker, S., Lyon, M., Roose, M.L., Ye, X.R., Fenton, R.D., Wanamaker, S., Lyon, M., Jang, C., Quinitio, C., Ikeda, J., Collin, M., Kacar, Y., Landry, B., Hubert, N., Laforest, M., Landry, J. and Ligonde, A. Development of EST Resources and New Genetic Markers for Caliberel States and Machington Navel Orange Callus - UCRCS08-2
Unpublished (2004) 749 bp mRNA linear EST 14-DEC-2004 Parent Washington Navel Orange Callus cDNA Library s sinensis cDNA clone UCRCS08-50B04-C8-1-5.g, mRNA Sciences A. California

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Tel: 909-78
Fax: 909-78
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Fax: 909-787-4437
Email: timothy.close@ucr.edu
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                                                                                                                                       CCTCAGTTATATAGTATCGCCGGACCAGACACAATGGATGAGATTAAATCAACGGCGGAG
                                                                                                                                                                                                              AACTCTTTCTACTCTCAGCTTATCTTACATGTTGCTTCTCATGGCTTCATGTAATCGCT
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                                                    ATTATGGATTGGTTATCAGTAGGACTTAATCACTTTCTTCCAGCGCAAGTAACACCAAAC
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  CCTCAGTTATACAATGTGGCTGGACCAGATGCAACTGCTGAGATTACGTCTGCAGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                           TGCAACAGTACAAGCTCCACTCCACTTCCGCCACCCAAGCCACTTTTGATCGGCATGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Site 1 ECORE, Site 2: XhoI, Parent Washington navel orange embryogenic Callus was established from undeveloped ovules of ca. 10 mm diameter young fruits under open pollination on Murashige-Skoog medium at 25oC with 16 h light in a tissue culture room. Embryogenic callus, globular and heart stage embryoids were pooled in approximately equal portions in RNAlater (Ambion), then RNA was extracted using TRIZOL Reagent (Invitrogen). Poly(A) RNA was purified from 500 microgram of total RNA using Qiagen Oligotex. A primary cDNA library was produced using a lambda ZAP XR cDNA Synthesis kit (Stratagene). These steps were performed by Xinrong Ye (Roose lab, UC Riverside). One million pfu from the primary library were mass excised to produce a phagemid population by Raymond Penton (Close lab, UC Riverside). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at DNA Landmarks (Landry, Hubert, Laforest, Landry, Ligonde). Chromatogram files were downloaded by FTP to UC Riverside (by Close), then processed at UC Riverside (by Wanamaker, Close lab) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were assembled, then chimeras were removed following manual inspection of assemblies (Close, Roose, Federici, Wanamaker, Lyon, Ye, Jang, Collin, Xacar, Ikeda, Quinitio). Sequences that survived all removal steps were submitted to GenBank."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Parent Washington Navel Orange Callus cDNA
Library UCRCS08-2"
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/lab_host="E. coli TJC121"
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db_xref="taxon:2711"
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Pred. No. 5.8e-71;
0; Mismatches 240;
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An Arabidopsis thaliana T-DNA mutagenized population flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Submitted (01-MAY-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA
                                                        Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B. Direct Submission
                                                                                                                                                Strizhov,N., Li,Y., Rosso,M.G., Viehoev Weisshaar,B. Weisshaar,B. High-throughput generation of sequence mutagenized Arabidopsis thaliana lines
                                                                                                                                                                                                                                                                                                                                                                                                                               Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis
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Arabidopsis thaliana T-DNA flanking
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                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 317)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                        AV556714 Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana cDNA clone SQ050d08F 3', mRNA sequence.
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/mol type="genomic DNA"
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'db_xref="taxon:3702"
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99.7%;
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Pred. No. 8.3e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Biotechnology Institute, 110
Saskatchewan, S7N OW9, Canada
Tel: 306 975 5267
Fax: 306 975 4839
Email: Raju.Datla@nrc-cnrc.gc.ca
High quality sequence stop: 542.
                                                                                                                                                                                                                                                                                                                                          26RDBNT_UP_011_F07_20JAN;
napus cDNA 5', mRNA seque
CN736070
CN736070.1 GI:65293887
EST:
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Brassica napus

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 542)

1 (bases 1 to 542)

Xiang,D., Venglat,P., Keller,G., Selvaraj,G. and Datla,R.

Kiang,D., Venglat,P., Keller,G., Selvaraj,G. and Datla,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Erika Asamizu
The First Laboratory for Plant Gene Res
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812,
Email: asamizu@kazusa.or.jp, URL:http:
Location/Qualifiers
                                                                            National Research Council of Canada
Plant Biotechnology Institute, 110 (
Saskatchewan, S7N 0W9, Canada
                                                                                                                                 Gene Expression Patterns during Brass
Unpublished (2004)
Contact: Raju Datla
Molecular and Developmental Genetics
                                                                                                                                                                                                                                                                                                                          Brassica napus (rape)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCACCTCTTTGCTTA
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/clone_lib="Arabidopsis thaliana green siliques Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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/mol_type="mRNA"
/ecotype="Columbia"
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mRNA sequence.
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                                                                                                                                                                                                                                                   CX076456 827 bp mRNA linear EST 14-DEC-2004 UCRCS08_50B04_b Parent Washington Navel Orange Callus cDNA Library UCRCS08-2 Citrus sinensis cDNA clone UCRCS08-50B04-C8-1-4.b, mRNA
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1 (bases 1 to 827)
Close, T.J., Roose, M.L., Ye, X.R., Fenton, R.D., Wanamaker, S., Lyon, M., Jang, C., Quinitio, C., Ikeda, J., Collin, M., Kacar, Y., Landry, B., Hubert, N., Laforest, M., Landry, J. and Ligonde, A.
                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Sapindales; Rutaceae; Citrus.
                                                                                                                                      Citrus sinensis
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/mol_type="mRNA"
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Pred. No. 1.8e-64;
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Contact: Timothy J. Close
Department of Botany & Plant Sciences
University of California
University of California
Riverside, CA 92521-0124, USA
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Seq primer: T7.
                                                                                             Interary Ocksober 2.

Interary Ocksober 2.

Interary Ocksober 2.

Interary Ocksober 2.

Interary Callus was established from undeveloped ovales of ca. 10 mm diameter young fruits under open ovales of ca. 10 mm diameter young fruits under open pollination on Murashige-Skoog medium at 250C with 16 h light in a tissue culture room. Embryogenic callus, globular and heart stage embryoids were pooled in approximately equal portions in RNAlater (Ambion), then RNA was extracted using TRIZOL Reagent (Invitrogen). Poly(A) RNA was purified from 500 microgram of total RNA using Qiagen Oligotex. A primary CDNA library was produced using a lambda ZAP XR CDNA Synthesis Kit (Stratagene). These steps were performed by Xinrong Ye (Roose lab, UC Riverside). One million pfu from the primary library were mass excised to produce a phagemid population by Raymond Fenton (Close lab, UC Riverside). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at DNA Landmarks (Landry, Hubert, Laforest, Landry, Ligonde). Chromatogram files were downloaded by FTP to UC Riverside (by Close), then processed at UC Riverside (by Wanamaker, Close lab) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were assembled, then chimeras were removed following manual inspection of assemblies (Close, Roose, Federicl, Wanamaker, Lyon, Ye, Jang, Collin, Kacar, Ikeda, Quinitio). Sequences that survived all removal steps were submitted to GenBank."
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/lab_host="B. coli TJC121"
/clone_lib="Parent Washington Navel Orange Callus cDNA
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/cultivar="Washington navel"
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Length
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Matches Query Match Best Local ( 337 ACAATGGATGAGATTAAATCAACGGCGGAGATTATGGATTGGATTATCAGTAGGACTTAAT Similarity CGCGGTGGCAAAACCGCGTTTGCGGTCGCCTTAAAGAAATTTGGGTACTCCTCGAATCTA CACTTTCTTCCAGCGCAAGTAACACCAAAACCTATCCAAATTTGCCCTCTCCGGCCATAGC GCAACTGCTGAGATTACGTCTGCAGCTGCAATCACAAATTGGTTATCTGAAGGACTCGGC GTTGCTTCTCATGGCTTCATTGTAATCGCTCCTCAGTTATACAATGTGGCTGGACCAGAT GTCTCTTCTCATGGCTTCATCCTCATCGCTCCTCAGTTATATAGTATCGCCGGACCAGAC Conservative 26.3%; Score 298; DB 8; I Pred. No. 4e-64; D; Mismatches 210; Indels Gaps 516 648 456 396 768 708

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                                                                                                                                   Department of Ecology, Evolution and Marine University of California, Santa Barbara Santa Barbara, CA 93106, USA Tel: 805 893 7813 Fax: 805 893 4724 Email: hodges@lifesci.ucsb.edu Seg primer: TTTTTTTTTTTTTTTTTTTTN (where
                                                                                                                                                                                                                                                            Hodges, S.A., Rensink, W., Buell, C. Nordborg, M. and Tomkins, J. Generation of ESTs from Aquilegia
                                                                                                                                                                                                                                                                                                                                                                                              EST1123539 Aquilegia pubescens cDNA clone DR932000
                                                                                                                                                                                                                                    Unpublished (2005)
Other_ESTs: EST1123540
                                                                                                                                                                                                                                                                                                                 Aquilegia formosa x Aquilegia pubescens
Aquilegia formosa x Aquilegia pubescens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
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                                                                                                                                                                                                                         Contact: Scott Hodges
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/tissue_type="mixed shoot and floral apical meristems, flower buds, leaves and roots" flower buds, leaves and roots" land T5 phage resistance)" /clone_lib="Aquilegia cDNA library" /note="Vector: pCMV SPORT6.1; Site_1: EcoRI; Site_2: NotI;
                                                               /organism="Aquilegia formosa
/mol type="mRA"
/db_xref="taxon.338618"
/clone="CO10D44"
                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        842 bp mRNA linear EST 02-AUG-2005 cDNA library Aquilegia formosa x Aquilegia CO10D44, mRNA sequence.
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   GATGATCGTGAATTAGTTAAGATCAAAGA
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were grown from seed in greenhouses at UC Santa Barbara. From these plants three sets of tissue were collected: 1) Small flower buds (<10 mm) and very young inflorescences (71 & 29% by weight respectively), 2) Medium (7-20 mm) and very yeight respectively) and 3) Shoot apical meristems. A fourth set of tissue was collected from plants of A. formosa. These plants were grown from seed in sand and at approximately 1 month root tissue and leaf tissue of various developmental stages were collected (4 & 16% by weight respectively). Total RNA was extracted from each set of tissue and pooled in the following proportions:

1.5X from sets 1 & 2, 1X from sets 3 & 4. From the pooled total RNA, mRNA was extracted and enriched for full-length messages and then normalized with proprietary methods by Invitrogen."

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Local Similarity
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                                                                                    CCAATGAGGAGATTCGTTGGTGGACTTGTTGTATCATTTTTGAAGGCTTATTTGGAAGGA 915
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                                                 CCAATGAGAACTTTTGGTTGGAGGAATTATGGTTGCATTTATGAAAGCATATATGGAAAAT 124
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Search completed: March 20, 2006, 16:53:01 Job time : 5146.9 secs

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123 GACTCTCGTGATTTAATGGCTATTAAAGA 95

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(without alignments)
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Ada71514 Rice gene	Abv07759 Human pro	Acn84831 Breast ca	Aall4805 Human bre	Acn51998 Cotton an	Ach19791 Human adu	Abv60941 Human pro	Abv08149 Human pro	Abt21705 Breast ca	Abx46069 Bovine ES	Aac76970 Human ORF	Abl34043 Human imm	Abv23838 Human pro	Abv29714 Human pro	Acn45312 Cotton pr	Acn51760 Cotton an	Acn48060 Cotton pr	Acn51676 Cotton an	Acl37108 Rice stre	Aad38087 Corn chlo	Aah41145 Chenopodi	Aad38081 Wheat chl	Acl27601 Rice abio	Acl32937 Rice abio	Aad38086 Wheat chl	Aah41135 Chenopodi

## RESULT 1 AAH41137 Chlorophyllase; transgenic plant; ds. AAH41137; AAH41137 standard; DNA; 1135 03-APR-2001. JP2001086990-A. Arabidopsis thaliana Arabidopsis thaliana chlorophyllase coding sequence #2 21-AUG-2001 (first entry) BP.

ALIGNMENTS

WPI; 2001-338421/36. P-PSDB; AAB99103. 20-SEP-1999; 20-SEP-1999; (KAGO ) KAGOME KK. 99JP-00266181 99JP-00266181.

DNA encoding chlorophyllase, useful for producing transgenic plants.

Claim 5; Page 12-14; 21pp; Japanese.

of a plant The present sequence is a chlorophyllase protein coding sequence. The chlorophyllase protein coding sequence can be used for the transformation

Query Match
Best Local Similarity 100
Matches 1135; Conservative Sequence 1135 BP; 331 A; 233 C; 247 G; 324 T; 0 U; 0 Other; 100.0%; Score 1135; DB 5; 100.0%; Pred. No. 9.4e-283; tive 0; Mismatches 0; Length 1135;

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Query Match
Best Local Sim:
Matches 1135;
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Hirschberg J,
Venkatesh TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel substantially purified nucleic acid molecule encoding a phytol kinase. The nucleic acid molecules and polypeptides of the invention may be useful in mediating tocopherol biosynthesis and in producing plants with increased drought resistance. The current sequence is that of the thale cress chlorophyllase 2 DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-AUG-2002;
05-AUG-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New phytol kinase polynucleotides, useful in mediating tocopherol biosynthesis and in producing plants with increased drought resis
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100.0%; ilarity 100.0%; Conservative 0
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J, Karunanandaa B,
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2003US-00634548.
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                                                                                               (first entry)
 Location/Qualifiers
                                                                                                                                          CDNA; 1216
                                                                         cDNA from vrllc.pk008.o21:fis clone.
                                                     chlorophyll degradation; plant cell
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                                                     senescence;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated polynucleotide encoding a plant chlorophyllase polypeptide, used to produce transformed plants that have controlled induction or postponement of senescence.
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                                                                                                                                                                                                                            AGCAGCTGTTGGTGGCTACGCCGGTGGAGGAAGGAAGTTATCCGGTGGTGATGCTCCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 48-49;
    CGCAAGTAACACCAAACCTATCCAAATTTGCCCTCTCCGGCCATAGCCGCGGTGGCAAAA
                                 GTTTCATTGTTCTTGCTCCTCAGTTATACACTGTGGCTGGACCAGATTCAAGCGAAGAGA
                                                                                                                                                  ATGGTTATCTTCTATAACTCTTTCTACTCCCAGCTCATCCAACACACATAGCCTCTCATG
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    /*tag= a
/product= "Grape chlorophyllase
/product= "Grape chlorophyllase
vrl1c.pk008.o21:fis clone"
/EC_number= "3.1.1.14"
/note= "CDS does not include stage."
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Pred. No. 2.2e-84;
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WPI; 2002-444102/47
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                                                                 04-OCT-2001; 2001WO-US031059
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                                                                                                                                                                          Tulipa gesneriana
                                                                                                                                                                                                 Tulip; chlorophyllase; chlorophyll degradation; plant cell senescence;
                                                                                                                                                                                                                 Tulip chlorophyllase cDNA from etplc.pk005.d16:fis clone.
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10-SEP-2002
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                                 PONT DE NEMOURS & CO E I.
                Cahoon RE,
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                                                  2000US-0238161P
                                                                                                                 /product= "Tulip chlorophyllase
etp1c.pk005.d16:fis clone"
/EC_number= "3.1.1.14"
                                                                                                                                                         Location/Qualifiers
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DR P-PSDB; AAE23782.

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PT An isolated polynucleotide encoding a plant chlorophyllase polypeptide, PT used to produce transformed plants that have controlled induction or PT postponement of senescence.

XX
PS Claim 5; Page 56-57; 69pp; English.
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The invention relates to plant chlorophyllase (EC 3.1.1.14) proteins and polynucleotides encoding such proteins. Chlorophyllase enzyme is involved in chlorophyll degradation in plant cell senescence. Sequences of the invention are used to produce a plant by transforming a plant cell with chlorophyllase and regenerating a plant from the transformed plant cell. They may also be used to transform cells. The plants that are produced can have economical importance as they can allow for the controlled induction or postponement of senescence. The present sequence is tulip chlorophyllase cDNA from etplc.pk005.dl6:fis clone. (Updated on 07-AUG-2003 to correct OS field.)

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Query Match
Best Local Sim:
Matches 474;
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GTTGCGAAGGATTATGGGCATTTGGACATGCTTGATGATGATACAAAAGGGATTAGAGGG 813
                                                                                                                                                                                          CTTGTGATCGGTTCGGGGGCTTGGTGAAACCGCTCGGAACCCATTATTCCCCACCGTGTGCA
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Pred. No. 8.9e-56;
0; Mismatches 287;
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                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                Matches
                                                                                                                                                                                                                                                 The invention relates to plant chlorophyllase (EC 3.1.1.14) proteins and polynucleotides encoding such proteins. Chlorophyllase enzyme is involved in chlorophyll degradation in plant cell senescence. Sequences of the invention are used to produce a plant by transforming a plant cell with chlorophyllase and regenerating a plant from the transformed plant cell. They may also be used to transform cells. The plants that are produced can have economical importance as they can allow for the controlled induction or postponement of senescence. The present sequence is grape chlorophyllase cDNA from vdblc.pk002.pl9:fis clone
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                             The invention relates to plant chlorophyllase (EC 3.1.1.14) proteins and polynucleotides encoding such proteins. Chlorophyllase enzyme is involved in chlorophyll degradation in plant cell senescence. Sequences of the invention are used to produce a plant by transforming a plant cell with chlorophyllase and regenerating a plant from the transformed plant cell.
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                          chlorophyllase
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                                                                                                                                                                                                                                                                                                                                                                                                                          postponement
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                                                                                                                                                                                                                                                                                                                  They may also be used to transform cells. The plants that are produced can have economical importance as they can allow for the controlled induction or postponement of senescence. The present sequence is corn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  isolated polynucleotide encoding a plant chlorophyllase polypeptide, ed to produce transformed plants that have controlled induction or
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ACTCCTCGAATCTAAAGATCTCGACATTGATCGGTATAGATCCAGTCGATGGAACAGGGA
                                                                        CAGTAGGACTTAATCACTTTCTTCCAGCGCAAGTAACACCAAACCTATCCAAATTTGCCC
                                                                                                                TCGCCGGACCAGACAATGGATGAGATTAAATCAACGGCGGAGATTATGGATTGGTTAT 382
                                                                                                                                              AGCTTATGTTGCATGTCTCTCATGGCTTCATCCTCATCGCTCCTCAGTTATATAGTA
                                                                                                                                                                        GGGAGTACCCGGTGATCCTGTTCCTACACGGCTACCTCGCCGTCAACTCCTTCTACTCCC
                                                                                                                                                                                    GAGATTATCCGGTGGTGATGCTCCTCCATGGTTACCTTCTCTATCAACTCCTTCTATTCTC
                                                                                                                                                                                                             CTTCTAGAGCTTCACCGTCTCCGCCAAAGCAGCTGTTGGTGGCTACGCCGGTGGAGGAAG
                   TCTCCGGCCACAGTCGCGGGGAAGGTGGCGTTCGCGCTTGGCGTTGGGCCACGCCAAGG
                                    TCTCCGGCCATAGCCGCGCTGGCAAAACCGCGTTTGCGGTCGCCTTAAAGAAATTTGGGT
                                                        CCACCGGGCTGCCGTCAACTCTGCCACTCGGCGTCCGCGCGAACCTAACCAAGGTGTCCA
                                                                                             TATCTGGGGCCGACACCACCGAGGAGATCAACTCAGCGGCGGCCGTCATCGACTGGCTAG
                                                                                                                                   AGCTGTTCGAGCACGTCGCCTCCCATGGCTTTATCGTCGTCGGACCTCAGCTGTACACCA
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                                                                                                                                                                                                                                                                                                         cDNA from csh3c.pk001.a9:fis clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Corn chlorophyllase protein
csh3c.pk001.a9:fis clone"
/EC_number= "3.1.1.14"
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(ZHOU/)
(KOVA/)
(SCRE/)
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          WPI; 2004-180133/17
                            Liu J,
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05-NOV-2001;
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                                                                                                                                                                                                     Unidentified
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                                              KOVALIC D K.
SCREEN S E.
TABASKA J E.
CAO Y.
                                                                                    LIU J.
                           Zhou Y,
                                                                                                                                                                                                                                                                                                                                                                  standard;
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plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance drought telerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator;
                                                                                                                                                                                                                                                                                                                 28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant full length insert polynucleotide segid 26342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant growth; plant development; seed
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oil; protein yield;
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The invention describes a recombinant DNA construct comprising a CC polynucleotide consisting of a sequence encoding an amino acid sequence cavailable in electronic form from the US patent office at Cftp.seqdata.usgto.gov/sequence.html?DocID:2004034888. The polynucleotide CC of the invention are also useful in physical arrays of molecules and as CI plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme cs. conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring CC increased resistance to plant disease, for producing galactomannan, CC lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake cor by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Pred. No. 5.2e-37;
0; Mismatches 325;
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211 CCGGTGGTGATGCTCCCATGGTTACCTTCTCTACAACTCCTTCTATTCTCAGCTTATG

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151 GCTTCACCGTCTCCGCCAAAGCAGCTGTTGGTGGCTACGCCGGTGGAGGAAGGA	Query Match 14.4%; Score 163.4; DB 6; Length 975; Best Local Similarity 54.3%; Pred. No. 1e-31; Matches 420; Conservative 0; Mismatches 341; Indels 12; Gaps	Sequence 975 BP; 250 A; 222 C; 256 G; 247 T; 0 U; 0 Other;	information supplied to Derwent by the European Patent Office	in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence	เล	with increased tolerance to abiotic stress. The present sequence is that	) }	detecting a profile of expressed polymucleotides in the plant cell	array or probes representative of the plant cell genome; and (b)	cell has been exposed, comprising: (a) contacting nucleic acid	The invention relates to identifying a stress condition to which a plant	Claim 144; SEQ ID NO 158; 577pp + Sequence Listing; English.	Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.		Harper JF, Kreps J, Wang X, Zhu T;		(SCRI ) SCRIPPS RES INST.	24-AUG-2000; 2000US-0227866F. 26-JAN-2001; 2001US-0264647F. 22-JUN-2001; 2001US-0300111F.	24-AUG-2001; 2001WO-US026685.	28-FEB-2002.	WO200216655-A2.	Arabidopsis thaliana.	Arabidopsis thaliana; plant; gene; stress; transgenic; ds.	Arabidopsis thaliana stress regulated gene SEQ ID NO 158.	21-JAN-2003 (first entry)	ABZ12353;	IIT 8 .2353 ABZ12353 standard; DNA; 975 BP.	849 AGTGAGATGAGAAGCTTTGTTGGTGGAATTGTGGTTTGCGTTTCTAAAG 896	853 AGACCAATGAGGAGATTCGTTGGTGGACTTGTTGTATCATTTTTGAAG 900	89 TIGCCCGGTTTTGTCGGGTTGTATGTGTGTAAGAACAGTAAAACGCAAAAAG	796	729 GCTACCAAGGGGCATTTCGTGGCTGCGGATTACGGACATATGGATATGTTGGACGATAAT 788

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                             15-SEP-2000;
22-JUN-2001;
                                                                                                                                                                    Arabidopsis thaliana.
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(SYGN ) SYNGENTA PARTICIPATIONS
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Matches 420;

Conservative

Score 163.4; DE Pred. No. 1e-31; 0; Mismatches 3

Length Indels

Gaps

GATTCAACAGCACCGCCAAAACCGGTGAGAATCACCTGTCCAACAGTCGCCGGAACTTAT 168
CCGGTGGTGATGCTCCTCCATGGTTACCTTCTCTACAACTCCTTCTATTCTCAGCTTATG 270

CCCGTCGTTTATTCTTCCATGGCTTTTATCTTCGCAACTACTTCTACTCTGACGTTCTT

228

TIGCACATCGCTTCTCATGGCTTCATCCTCATCGCTCCTCAGCTTTATATAGTATCGCCGGA

Query Match Best Local Similarity

14.4%;

DB 6; 31; 341;

975; 12;

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TCGAATCTAAAGATCTCGACATTGATCGGTATAGATCCAGTCGATGGAACAGGGAAAAGGG 567

 CTCAAAGCTCACCTACCAACTTCGGTAAATGCTAATGGAAAATACACCTCACTCGTGGGC

408

CTTAATCACTTTCCTTCCAGCGCAAGTAACACCAAACCTATCCAAATTTGCCCCTCTCCGGC

CCAGACACAATGGATGAGATTAAATCAACGGCGGAGATTATGGATTAGGTTATCAGTAGGA 390

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CC cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat. The capression of genes of the invention was upregulated or downregulated in CC Arabidopsis plants infected with the comycete Peronospora parasitica, CC indicating that they play a role in defence mechanisms. The genes of the invention are regulated by RPP7 or RRP8 which act via unconventional CC signalling cascades, or by the RPP4-dependent pathway. The invention also CC relates to polypeptides encoded by the pathogen infection-related genes; CC promoter motifs from pathogen infection-related genes (ADG88243-ADG88327) (2) expression cassettes, host cells and pathogen-resistant transgenic CC plants and their progeny comprising a polynuclectide of the invention; CC and a method of identifying a plant cell infected with a pathogen. The CC polynucleotide sequences and methods of the invention are useful for CC identifying plants infected with a pathogen, and for conferring CC resistance to pathogens such as comycetes, fungi, bacteria, viruses, comparasitica infection. Note: The sequence data for this patent CC Arabidopsis thaliana gene whose expression is altered in response to CC Peronospora parasitica infection. Note: The sequence data for this patent CC did not form part of the printed specification, but was obtained in CC electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to 691 Arabidopsis thaliana genes (ADG87559-ADG87557)) whose expression is altered in response to pathogen infection, and to homologues of these genes from other plants or fungi, especially from maize, soybean, barley, alfalfa, sunflower, canola (ollseed rape),
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(GLAZ/)
(WANG/)
(DANG/)
Sequence 975 BP;
                                            ftp.wipo.int/pub/published_
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250 A; 222 C; 256 G; 247 T; 0 U; 0 Other;
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(DANG/)
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22-JUN-2001;
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ADG87557}) whose expression is altered in response to pathogen infe
                                                                              Novel isolated to plants, and
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 87557}) whose expression is altered in response to pathogen infection,
to homologues of these genes from other plants or fungi, especially
m maize, soybean, barley, alfalfa, sunflower, canola (oilseed rape),
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                                                                                                                                                                                                                                                                                                                                                                             infection-related gene; plant; Peronospora parasitica;
nechanism; RPP7; RRP8; pathogen resistance; transgenic
; fungus; bacterium; virus; nematode; insect; aphid; ge
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Best Local S
Matches 420
                                                                                                                                                                                                                                                                                                                                         Sequence 1188
                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding chlorophyllase, useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP2001086990-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana chlorophyllase coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KAGO ) KAGOME KK.
                                                                                                                                                                                                                                                                                                                                                                        e present sequence is a chlorophyllase protein
lorophyllase protein coding sequence can be us
                                                                                                                                                                                                                                                                                                                                                               a plant
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                                                                                                                                                                                                                                                                                                                                                                                                         3; Page 10-11; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                        Similarity
TCGAATCTAAAGATCTCGACATTGATCGGTATAGATCCAGTCGATGGAACAGGGAAAGGG
                     CACAGCCGCGGTGGGAAAACGGCGTTTGCGGTTGCGCTAGGCCATGCCGCAACATTAGAC
                                           CATAGCCGCGGTGGCAAAACCGCGTTTGCGGTCGCCTTAAAGAAATTTG---GGTACTCC
                                                                 CTCAAAGCTCACCTACCAACTTCGGTAAATGCTAATGGAAAATACACCTCACTCGTGGGC
                                                                                  CTTAATCACTTTCTTCCAGCGCAAGTAACACCAAACCTATCCAAATTTGCCCTCTCCGGC
                                                                                                              CCGGGAGGGCAAGTGGAAGTGGACGATGCTGGAAGTGTGATAAACTGGGCATCGGAAAAC
                                                                                                                                  CCAGACACAATGGATGAGATTAAATCAACGGCGGAGATTATGGATTGGTTATCAGTAGGA
                                                                                                                                                          AACCACATCGCTTCGCATGGTTACATTCTTGTAGCCCCACAGTTGTGCAAATTATTGCCG
                                                                                                                                                                          TIGCATGTCTCTCATGGCTTCATCCTCATCGCTCCTCAGTTATAGTATCGCCGGA
                                                                                                                                                                                                     CCCGTCGTTTATTCTTCCATGGCTTTATCTTCGCAACTACTTCTACTCTGACGTTCTT
                                                                                                                                                                                                                    CCGGTGGTGATGCTCCATGGTTACCTTCTCTACAACTCCTTCTATTCTCAGCTTATG
                                                                                                                                                                                                                                                  GATTCAACAGCACCGCCAAAACCGGTGAGAATCACCTGTCCAACAGTCGCCGGAACTTAT
                                                                                                                                                                                                                                                                       standard; DNA; 1188
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1.1e-31;
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                                                                                                                                                                                                                                                                                                                  Length 1188;
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DX Thale
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                                                                                                                                                                                                                                                                                     New phytol kinase polynucleotides, useful biosynthesis and in producing plants with
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Venkatesh TV;
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05-AUG-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Norris SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MONS ) MONSANTO TECHNOLOGY LLC
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2003US-00634548.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chlorophyllase
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Moshiri F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant; drought resistance;
                                                                                                                                                                                                                                                                                        in mediating tocopherol increased drought resistance.
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Stein JC, Vale
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The invention relates to a novel substantially purified nucleic acid molecule encoding a phytol kinase. The nucleic acid molecules and polypeptides of the invention may be useful in mediating tocopherol biosynthesis and in producing plants with increased drought resistance. The current sequence is that of the thale cress chlorophyllase 1 DNA of

and

Claim 23; SEQ ID NO 18; 189pp; English.

Sequence 1188 BP; 327

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                                       enzyme; gene;
                                                                            Soybean chlorophyllase cDNA from sfll.pk0046.f8 clone.
                                                                                                          10-SEP-2002
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                                                     chlorophyllase;
                                                                                                                                                             standard;
                                                                                                                                                                                                                                                AGATTCGTTGGTCGTTGTTGTATCATTTTTGAAGGCTTATTTGGAAGGAGA
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                                                                                                                                                             CDNA; 1174
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                                                     chlorophyll
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                                                   degradation;
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Best Local S
Matches 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to plant chlorophyllase (EC 3.1.1.14) proteins and polynucleotides encoding such proteins. Chlorophyllase enzyme is involved in chlorophyll degradation in plant cell senescence. Sequences of the invention are used to produce a plant by transforming a plant cell with chlorophyllase and regenerating a plant from the transformed plant cell. They may also be used to transform cells. The plants that are produced can have economical importance as they can allow for the controlled induction or postponement of senescence. The present sequence is soybean chlorophyllase cDNA from sfll.pk0046.f8 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An isolated polynucleotide encoding a plant chlorophyllase polypeptide, used to produce transformed plants that have controlled induction or postponement of senescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1174 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 52; 69pp; English.
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DB; AAE23779.
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                   AATTIGGGTACTCCTCGAATCTAAAGATCTCGACATTGATCGGTATAGATCCAGTCGATG
                                                                                  AATTTGCCCTCTCCGGCCATAGCCGCGGTGGCAAAACCGCGTTTGCGGGTCGCCTTAAAGA
                                                                                                                                 GGTTATC---AGTAGGACTTAATCACTTTCTTCCAGCGCAAGTAACACCCAAACCTATCCA
                                                                                                                                                                       GTGTACGGTCTATGTTGGAACCTGGTGATGAAGTTAAATTTGCAGGGAAAGTTGTGGATT
                                                                                                                                                                                                  TCGCCGGACC-----AGACACAATGGATGAGATTAAATCAACGGCGGAGATTATGGATT
                                                                                                                                                                                                                                              AGCTTATGTTGCATGTCTCTCATGGCTTCATCGTCATCGCTCCTCAGTTATATAGTA
                                                                                                                                                                                                                                                                                       GCTCATACCCTGTAATATTGTTCTGCCATGGATTTTCCCTTCGCAATAGCTACTACTCTG
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                                                        AATTGGTTTTATCAGGTCACAGCAAGGGTGGCAAAACTGTATTTGCTGTGGCACTTGGTT
                                                                                                              GGCTAGCCGAGGAGGGGCTTCAACCTCTGCTTCCAGAGAATGTTGAAGCCAAATTGGATA
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                                                                                                                                                                                                                                                                                                                                              CATCCAATGCTTCCTCCTCACCTCCAAAACCATTGTTAATCTTTACACCAACCGTGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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/product= "Soybean chlorophyllase
sfl1.pk0046.f8 clone"
/EC_number= "3.1.1.14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
 --- Amanctancetcangtitteageactagtaggeatagaceetgtggetg
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 151; DB 6;
Pred. No. 1.8e-28;
0; Mismatches 330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1174;
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GAACAGGGAAAGGGAAACCAAACCCCTCCTCCGGTGTTGGCTTACCTTCCAAACTCATTTG

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RESULT 14
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The invention relates to plant chlorophyllase (EC 3.1.1.14) proteins polynucleotides encoding such proteins. Chlorophyllase enzyme is invo
                                                                              Claim 5; Page 59;
                                                                                                                              An isolated polynucleotide encoding a plant chlorophyllase polypeptide, used to produce transformed plants that have controlled induction or postponement of senescence.
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DB; AAE23784.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGACACCTGGCTTAATTGGGTCAATATTGTCAAATTGTATATGCAAGGATGGGAAGGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Wheat chlorophyllase wlein.pk0058.a4:fis clone" /EC_number= "3.1.1.14"
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                                                                              69pp; English
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Best Local S
Matches 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in chlorophyll degradation in plant cell senescence. Sequences of the invention are used to produce a plant by transforming a plant cell with chlorophyllase and regenerating a plant from the transformed plant cell. They may also be used to transform cells. The plants that are produced can have economical importance as they can allow for the controlled induction or postponement of senescence. The present sequence is wheat chlorophyllase cDNA from wlein.pk0058.a4:fis clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1242 BP; 266 A; 382 C; 343 G; 251 T; 0 U; 0 Other;
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357; Conserv
      CATTTCGTTGCGAAGGATTATGGGCATTTGGACATGCTTGATGATGA
                                                                                                                                                                                                   ANACANACCCCTCCTCCGGTGTTGGCTTACCTTCCANACTCATTTGACCTAGACANAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTTCGGGTGACGCAGAGACATCGCCGCGGCAGCCAAGGTGGCAGACTGGCTCCCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACCAGACACAATGGATGAGATTAAATCAACGGCGGAGATTATGGATTGGTTATCAGTA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGCACGTCGCATCCCACGGCTTCATCATTGTCGCGCCCCAGTTCAGCATCAGTATCATA 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGTGGCCATGCTCTTGCACGGCTTCTTCCTCCATAACCACTTCTACGAACACCTTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTGCACCTCCCGGAGTGAATCACCGAGAGTTCTTTCGGGAATGTCAAGGTCCAGCATGG
                                                                                                     TCCCAGCTCCAGCCCAAGATCCTCACCTACGAGCCGTCCTTCCGTCGTAGG---CGATG
                                                                                                                                                                                                                                                                                                                                    GGCCATAGCCGCGTGGCAAAACCGCGTTTGCGGTCGCCTTAAAGAAATTTGGGTACTCC
                                                                                                                                                                                                                                                                                                                                                                                                 GGACTTAATCACTTTCTTCCAGCGCAAGTAACACCAAACCTATCCAAATTTGCCCTCTCC 447
                                                                                                                                    CCTATACTTGTGATCGGTTCGGGGGCTTGGTGAAACCGCTCGGAACCCATTATTCCCCACCG
                                                                                                                                                                                                                                     ---CAGCTAACCTTCTCCGCGCTCATCGGACTCGACCCCGTCGCCGGCACGGGAAGTCC
                                                                                                                                                                                                                                                                  TCGAATCTAAAGATCTCGACATTGATCGGTATAGATCCAGTCGATGGAACAGGGAAAGGG
                                                                                                                                                                                                                                                                                                   GGCCACAGCCGAGGAGGCCACACGGCTTTCTCCCTGGCCTTGGGGCACGCCAAGACC---
                                                                                                                                                                                                                                                                                                                                                                    GGCCTCCCGTCCGTGCTGCCCAAAGGCGTCGAGCCGGAGCTCTCGAAGCTCGCCTTGGCC
                                       TGCGCACCCAAGGACGTGAACCACGCCGAGTTCTACCGCGAGTGCAGGCCGCCCTGCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 148.2;
Pred. No. 9.
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ID AAD38
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XX Soybe
Glycine max
                                                                                                                                                             AAD38078 standard;
                           enzyme;
                                           Soybean; chlorophyllase; chlorophyll degradation;
                                                                        Soybean
                                                                                                     10-SEP-2002
                           gene;
                                                                      chlorophyllase cDNA from sflln1.pk002.ml0:fis
                                                                                                     (first
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                                                                                                                                                             CDNA; 1104
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                                                                                                                                                              ВP
                                           plant cell
                                                                        clone
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senescence;

764

TACTTTGTGACCAAGGACTACGGGCATCTGGACATGCTGGACGACGA

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Query Match
Best Local S
Matches 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to plant chlorophyllase (EC 3.1.1.14) proteins and polynucleotides encoding such proteins. Chlorophyllase enzyme is involved in chlorophyll degradation in plant cell senescence. Sequences of the invention are used to produce a plant by transforming a plant cell with Chlorophyllase and regenerating a plant from the transformed plant cell. They may also be used to transform cells. The plants that are produced can have economical importance as they can allow for the controlled induction or postponement of senescence. The present sequence is soybean chlorophyllase cDNA from sflln1.pk002.m10:fis clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated polynucleotide encoding a plant chlorophyllase polypeptide, used to produce transformed plants that have controlled induction or postponement of senescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 53; 69pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-OCT-2000; 2000US-0238161P
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                                                                                                    CCCTCTCCGGCCATAGCCGCGGTGGCAAAACCGCGTTTGCGGTCGCCTTAAAGAAATTTG
  GGTACTCCTCGAATCTAAAGATCTCGACATTGATCGGTATAGATCCAGTCGATGGAACAG
                                                                                                                                                        TAGCTGAGGAGCTTCAACATTTGCTTCCAGAGAACGTTGAAGCCAATTTGGACAAACTGG
                                                                                                                                                                                      TATCAGTAGGACTTAATCACTTTCCTTCCAGCGCAAGTAACACCAAACCTATCCAAATTTG
                                                                                                                                                                                                                                                                                                                                                                                                     GCGCATACCCTGTAATATTGTTCGTCCATGGCTTTTTCATTCGCAATTTCTACTACTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCTAGAGCTTCACCGTCTCCGCCAAAGCAGCTGTTGGTGGCTACGCCGGTGGAGGAAG
                                                                                                                                                                                                                                          ATGGGCTTCCTATGTATGGACCCACTGAAGTGGAATATGCAGGAAAAGTTGCGGATTGGA
                                                                                                                                                                                                                                                                                                                        AGCTCCTAGCCCACATAGTCTCACATGGATTCATAATCGTTGCTCCTCAACTGTTTTCCA
                                                                                                                                                                                                                                                                                                                                                           AGCTTATGTTGCATGTCTCTTCATGGCTTCATCCTCATCGCTCCTCAGTTATATAGTA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGATTATCCGGTGGTGATGCTCCTCCATGGTTACCTTCTACAACTCCTTCTATTCTC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATCCAGTGCTTCCTCACCTCCAAAACCATTGCTAATTTTTACACCAACTGTTCCTG
                                                                               TTCTATCAGGTCACAGTAGGGGTGGGAAAACTGTATTTGCTGTGGCTCT--
                                                                                                                                                                                                                                                                                TCGCCGGACC---AGACACAATGGATGAGATTAAATCAACGGCGGAGATTATGGATTGGT 379
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sflln1.pk002.m10:fis clone"
/EC_number= "3.1.1.14"
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26. .967
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53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 145.4; DB 6; Pred. No. 4.9e-27;
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US08A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US08A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

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	7003, Ap	60960, A	3830, Ap	8140, Ap	3821, Ap	Sequence 1, Appl:	78, Appl	11234, A	2016, Ap	29732, A	23827, A	93, Appl	6541, Ap	-	6457, Ap	27, Appl	166593,	34072, A	68342, A	15, Appl	41107, A	020247 5

## ALIGNMENTS

RESULT 1  US-10-634-548-19  Sequence 19, Application US/10634548  Sequence 19, Application WS/10634548  Sement indexmarked in the US20040045051Alris, Susan R  APPLICANT: Lincoln, Kim APPLICANT: Valentin, Henry E. APPLICANT: Valentin, Henry E. APPLICANT: Valentin, Henry E. APPLICANT: Valentin, Henry E. APPLICANT: Valentin, Tymmagondlu V. TITLE OF: INVENTION NUMBER: US/10/634,548  CURRENT APPLICANT: Nonders: 200-08-05  FILE REPERENCE: Ren-01-15  CURRENT APPLICANTION NUMBER: US/10/634,548  CURRENT APPLICANTION N
4-548-19 acton No. US20040045051A1ris, Susan R CANT: Lincoln, Kim CANT: Lincoln, Kim CANT: Hartsuyker, Karen Kindle CANT: Hartsuyker, Karen Kindle CANT: Weinkatesh, Tyamagondlu v. CONT: Venkatesh, Tyamagondlu v. COP'INVENTION: Tocopherol blosynthesis related genes and used thereof REFERECE: Ren-01-125 CANT: Venkatesh, Tyamagondlu v. OP'INVENTION: Tocopherol blosynthesis related genes and used thereof REFERECE: Ren-01-125 CANT: Venkatesh, Tyamagondlu v. OP'INVENTION: Tocopherol blosynthesis related genes and used thereof REFERECE: Ren-01-125 CANT: Venkatesh, Tyamagondlu v. OP'INVENTION NUMBER: US/10/634,548 NT FILING DATE: 2003-08-05 APPLICATION NUMBER: US 60/400,689 FILING DATE: 2003-08-05 APPLICATION N

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RESULT 2
US-10-381-123-3
; Sequence 3, Application US/10381123
; Publication No. US20050081263A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Company
; TITLE OF INVENTION: Chlorophyllases
; FILE REFERENCE: BB1477 PCT
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CURRENT FILING DATE: 2003-03-21;
PRIOR APPLICATION NUMBER: PCT/US01/31059;
PRIOR FILING DATE: 2001-10-04
PRIOR PLICATION NUMBER: 60/238,161;
PRIOR FILING DATE: 2000-10-05;
NUMBER OF SEQ ID NOS: 30;
SEQ ID NO 3;
SEQ ID NO 3;
LENGTH: 1216
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; ORGANISM: Vitis
US-10-381-123-3
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Best Local
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Local Similarity 63.9%;
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                                                GGCATTTGGACATGCTTGATGATGATACAAAAGGGATTAGAGGGGAAGAGTTCTTATTGTT
                                                                                                 ATGAGGACTTCTTTAAAGAATGCCGTGAACCAGCTTGTTATTTTCTTGCCAAGGACTATG
                                                                                                                    ACCGAGAGTTCTTTCGGGAATGTCAAGGTCCAGCATGGCATTTCGTTGCGAAGGATTATG
                                                                                                                                                GTTTGGGTGAAAGGAAAAGGAACCCTCTGTTCCCTCCTTGTGCCCCCAAGGGCGTAAACC
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   TGTGTAAAAATGGGAAGTCTAGAGAACCCATGAGGAGGTTTGTTGGAGGCATTGTGATTG
                TGTGTAAGAATGGTGAAGAGAGGAGACCAATGAGGAGATTCGTTGGTGGACTTGTTGTAT
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Sequence 13, Application US/10381123
Publication No. US20050081263A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
TITLE OF INVENTION: Chlorophyllases
FILE REFERENCE: BB1477 PCT
CURRENT APPLICATION NUMBER: US/10/381,123
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: PCT/US01/31059
PRIOR APPLICATION NUMBER: PCT/US01/31059
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SEQ ID NO 13
LENGTH: 1444
TYPE: DNA
ORGANISM: Gesneriana
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PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 30
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  CCTCCCGGAGTGAATCACCGAGAGTTCTTTCGGGAATGTCAAGGTCCAGCATGGCATTTC
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                                                                                                                                                                                                                                                                                                               AGCCGCGGTGGCAAAACCGCGTTTGCGGTCGCCTTAAAGAAATTTGGGTACTCCTCGAAT 513
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                                      TTAGTTATCGGAACAGGTTTAGGTGAATTGAAGAGGAACCTATTTGCC-----TGTGCC 723
                                                                           crigrearcecircegecriegieaaaccecregaacceariarreceaccerereca 693
                                                                                                                  ACCAATCCTCCTGTACTGAATTATATCCCTCACTCTTTGGAACT---CAAGATGCCGTCA
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; ORGANISM: Vitis sp
US-10-381-123-1
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FILE REFERENCE: BB1477 PCT
CURRENT APPLICATION NUMBER: US/10/381,123
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: PCT/US01/31059
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR FILING DATE: 2000-10-05
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Publication No. US20050081263A1
GENERAL INFORMATION:
APPLICANT: B.I. du Pont de Nemours and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 987
                                    578
437
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                                                                                                                                                                                                                                                                                                               203 GAATTCAAGAGATCAAATCAGCAGCAGCAGTCACAAATTGGCTATCCTCAGGCCTTCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                 278 TCTCTTCTCATGGCTTCATCCTCATCGCTCCTCAGTTATATAGTATCGCCGGACCAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 TGATGCTCCATGGTTACCTTCTCTACAACTCCTTCTATTCTCAGCTTATGTTGCATG
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TTCCCAAAATCCTAACCTATGTTCCTCATTCCTTCAATCTAG---CAATCCCAGTTTGCG
                                  CTCCTCCGGTGTTGGCTTACCTTCCAAACTCATTTGACCTAGACAAAACGCCTATACTTG
                                                                                                            GAGGGGGAAAGACAGCATTTGCTCTGGCACTAGGGTATGCTGATACATCC-----CTCA
                                                                                                                                                                                          GCGGTGGCAAAACCGCGTTTGCGGTCGCCTTAAAGAAATTTGGGTACTCCTCGAATCTAA
                                                                                                                                                                                                                                   CTGTGCTCCCAGAAAATGTGAAAACCAGACCTACTCAAGCTTGCTCTTTCAGGCCACAGCA
                                                                                                                                                                                                                                                           ACTITICTTCCAGCGCAAGTAACCACAAACCTATCCAAATTTTGCCCTCTCCGGCCATAGCC
                                                                                                                                                                                                                                                                                                                                                  CAATGGATGAGATTAAATCAACGGCGGAGATTATGGATTGGTTATCAGTAGGACTTAATC 397
                                                                                                                                                                                                                                                                                                                                                                                          TTTCTTCCCATGGATTCATTGTGGTGGCTCCTCAGTTATACGGACTATTACCTCCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTGTTTCTTCATGGCTTCGAGCTCCGCAACACCTTCTACACTCAGCTCCTTCAACTCA
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                                                                           ACTTCTCAGCCCTACTAGGACTAGACCCTGTTGGTGGGTTGAGTAAATGTTGCCAAACAG
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ilarity 56.3%;
Conservative
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Pred. No. 9.6e-54;
0; Mismatches 411;
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Gaps

142

82 217

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637 436 577 376

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APPLICANT: E.I. du Pont de Nemours and Company TITLE OF INVENTION: Chlorophyllases FILE REFERENCE: B91477 PCT
CURRENT APPLICATION NUMBER: US/10/381,123
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: PCT/US01/31059
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR FILING DATE: 2000-10-05
NUMBER: OF SEQ ID NOS: 30
SOPTWARE: Microsoft Office 97
SEQ ID NO 5
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                                                                                                                           Matches 449;
                                                                                                                                                   Query Match
                                                                                                                                                                                   LENGTH: 1302
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                       Local Similarity
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 AGCTTATGTTGCATGTCTCTCATGGCTTCATCCTCATCGCTCCTCAGTTATATAGTA 322
                                                 GAGATTATCCGGTGGTGATGCTCCTCCATGGTTACCTTCTCTACAACTCCTTCTATTCTC
                                                                          AAAAAAAAAAAAAAAAAA 987
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                                                                                                                           Conservative
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                                                                                                                                      Score 201.6; DB 9;
Pred. No. 6.7e-44;
                                                                                                                          Mismatches 364;
                                                                                                                                    6.7e-44;
                                                                                                                                                Length 1302;
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 Best Local Similarity
           Query Match
                                                                                      TYPE: DNA
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                                           ATGATCGTGAATTAGTTAAGATCAAAGATGGGTGTCACGAGG 958
                                                                                                                                                                            CAATGAGGAGATTCGTTGGTGGACTTGTTGTATCATTTTTGAAGGCTTATTTGGAAGGAG
                                                                                                                                                                                                                                                                                                                                                         CGCCAGCGTGCCACCTGGTGGTCAGGGACTACGGGCACACGGACATGATGGACGACGACA
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ACGCCGCGGCGATGGACÁGCATCACGGCGCGGGCCGGACCAGG 1059
                                                                                                                     CCATGCGCCGCTTCGTGGCCGGCGCCACCGTCGCGTTCCTCAAGAAATGGGTGGCTGGGG
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Sequence 140359, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and FILICATE: 38-21153223)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 140359
LENGTH: 2439
; OTHER INFORMATION: Clone ID: MRT4577_59490C.1 US-10-425-115-140359
                                                    ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                         Other Molecules Associated With
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17.8%;

Score 201.6; DB 8 Pred. No. 9.6e-44;

8

Length 2439;

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RESULT 7
US-10-424-599-86252
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                                                                                                                                                             Sequence 86252, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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                                                                      Associated With
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                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Kovalic, David K.

APPLICANT: Kovalic, David K.

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 39-21(5313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 26342

LENGTH: 1125
                                                       ; OTHER INFORMATION: US-10-425-114-26342
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US-10-425-114-26342
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SEQ ID NO 86252
LENGTH: 796
TYPE: DNA
ORGANISM: Glycine max
FERTURE:
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26342, Application US/10425114 Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.4
Best Local Similarity 65.9
Matches 288; Conservative
                                                                                     TYPE: DNA
ORGANISM: Brassica
FEATURE:
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                                                                      Clone ID:
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   Score
Pred.
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Pred. No. 1.2e-39;
0; Mismatches 149;
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   184;
   3.9e-39;
                    Length 1125
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With

748 184 889 124 628 67

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APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Asso

FILE REFERENCE: 38-21(5322))B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT APPLICATION DATE: 2003-04-28

NUMBER OF SEQ ID NO 131410

LENGTH: 635
                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-10-424-599-131410
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                                                                                                                                                          APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION UNMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 158
LENGTH: 975
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                                                                                                              ; ORGANISM: Arabidopsis thaliana US-09-938-842A-158
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US-09-938-842A-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 158, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
                                                  Query Match
Best Local Similarity
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OTHER INFORMATION: unsure at FEATURE:
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                                 Score 163.4; DB 3
Pred. No. 1.5e-33;
0; Mismatches 341
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Pred. No. 5.1e-38;
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PL
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPIJOO-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                   Sequence 158, Application US/09938842A Publication No. US20040009476A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              AGATTCGTTGGTGGACTTGTTGTATCATTTTTGAAGGCTTATTTTGGAAGGAGA
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; SEQ ID NO 158
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Arabidopsis tUS-09-938-842A-158
; Sequence 18, Application US/10634548; Publication No. US20040045051A1; GENERAL INFORMATION: ; APPLICANT: No. US20040045051A1ris, Su; APPLICANT: Lincoln, Kim; APPLICANT: Abad, Mark Scott; APPLICANT: Eilers, Robert
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APPLICANT: Hirabberg, Joseph
APPLICANT: Karunanandaa, Balasulojini
APPLICANT: Karunanandaa, Balasulojini
APPLICANT: Karunanandaa, Balasulojini
APPLICANT: Weshiri, Farhad
APPLICANT: Vesentin, Joshua C.
APPLICANT: Vesentin, Henry E.
FILLE REFERENCE: Ren-01-125
CURRENT APPLICATION NUMBER: US/10/634,548
CURRENT APPLICATION NUMBER: uS/10/634,548
CURRENT FILING DATE: 2003-08-05
PRIOR FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 79
PRIOR FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 79
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LENGTH: 1188
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Pred. No. 1.7e-33;
0; Mismatches 341;
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CURRENT APPLICATION NUMBER: US/10/381,123
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: PCT/US01/31059
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
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US-10-381-123-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: E.I. du Pont de Nemours and Company
TITLE OF INVENTION: Chlorophyllases
FILE REFERENCE: BB1477 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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Local Similarity 55.0%;
les 433; Conservative
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AAGGTCCAGCATGGCATTTCGTTGCGAAGGATTATGGGCATTTTGGACATGCTTGATGATG
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                                                                             CATTATTCCCACCGTGTGCACCTCCCGGAGTGAATCACCGAGAGTTCTTTCGGGAATGTC 733
                                                                                                                                                                                                                                                                                                                                                                      AATTTGCCCTCTCCGGCCATAGCCGCGGTGGCAAAACCGCGTTTGCGGTCGCCTTAAAGA
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                                                        TTTTTATTCCACCATGTGCTCCTGATGGGGTGAACCATAAGGAGTTTTTCAATAAGTGCA 687
                                                                                                                                                     ACCTAGACAAAAACGCCTATACTTGTGATCGGTTCGGGGGCTTGGTGAAACCGCTCGGAACC
                                                                                                                                                                                                       GCCCATGTAAATCTTGCGAAACATTTCCTCCTATTCTCACTGGCATGTCCCAATCCTTCA
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                                                                                                                               ATTTGAACATA---CCCATTGTTGTAATTGGCACTGGGCTAGGCCCAGAGAAGGCTAATT 627
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Pred. No. 4.1e-30;
0; Mismatches 330;
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Sequence 17, Application US/10381123
Publication No. US20050081263A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
TITLE OF INVENTION: Chlorophyllases
PILE REFERENCE: B81477 PCT
CURRENT APPLICATION UNMBER: US/10/381,123
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: PCT/US01/31059
PRIOR APPLICATION UNMBER: PCT/US01/31059
PRIOR APPLICATION UNMBER: 60/238,161
PRIOR PILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1242
; TYPE: DNA
; ORGANISM: Triticum
US-10-381-123-17
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US-10-381-123-17
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SEQ ID NO 17
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Best Local
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                             TCCCAGCTCCAGCCCAAGATCCTCACCTACGAGCCGTCCTTCGGCATGG----CGATG
                                                                                                                                       TCGAATCTAAAGATCTCGACATTGATCGGTATAGATCCAGTCGATGGAACAGGGAAAGGG
                                                                                                                                                                                                                                                                                     GECCTCCCGTCCGTGCTGCCCAAAGGCGTCGAGCCGGAGCTCTCGAAGCTCGCCTTGGCC
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                                                                                                                                                                                                  GGCCACAGCCGAGGAGGCCACACGGCTTTCTCCCTGGCCTTGGGGCACGCCAAGACC---
                                                                                                                                                                                                                                      GGCCATAGCCGCGGTGGCAAAACCGCGTTTGCGGTCGCCTTAAAGAAATTTGGGTACTCC
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                                                                                                                                                                                                                                                                                                                                                                        CCTTCGGGTGACGCAGAGGACATCGCCGCGGCAGCCAAGGTGGCAGACTGGCTCCCCGAC 412
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                                                                                                              ---CAGCTAACCTTCTCCGCGCTCATCGGACTCGACCCCGTCGCCGGCACGGGGAAGTCC
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Pred. No. 2.5e-29;
0; Mismatches 278;
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; TYPE: DNA
; ORGANISM: Glycine
US-10-381-123-9
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US-10-381-123-9
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PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,161
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/10381123
Publication No. US20050081263A1
GENERAL INFORMATION:
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Best Local Similarity 53.8%;
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TITLE OF INVENTION: Chlorophyllases
FILE REFERENCE: BB1477 PCT
CURRENT APPLICATION NUMBER: US/10/381,123
CURRENT FILLING DATE: 2003-03-21
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ACAAAACGCCTATACTTGTGATCGGTTCGGGGGCTTGGTGAAACCGCTCGGAACCCATTAT
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                                                                   CTĂĂĂTATTGTAGĂĂĊAĆGTĆĊTĆATATTCTCAĆTGGĆAAGĆĆĂCGGTĆCTTTĠATTT--
                                                                                                            GGAAAGGGAAACAAACCCCTCCTCCGGTGTTGGCTTACCTTCCAAACTCATTTGACCTAG
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Pred. No. 1.4e-28;
0; Mismatches 341;
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1: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

11: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

12: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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       1 6 US-09-925-065A-605854

1 7 US-10-330-773-37

6 US-09-925-065A-343968

6 US-09-925-065A-343967

18 US-11-122-329-76

19 US-11-122-329-76

10 US-09-925-065A-84331

10 US-09-925-065A-84331

10 US-09-925-065A-84332

10 US-11-051-720-1711

11 US-11-043-806-516

12 US-11-043-806-516

12 US-11-043-806-516

13 US-10-750-185-31978

14 US-10-750-185-31978

15 US-10-750-623-31978

17 US-11-08-172-690

18 US-10-750-623-31978

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5830.519 Million cell updates/sec
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Sequence 37, Appl
Sequence 343967,
Sequence 91, Appl
Sequence 12837, A
Sequence 12837, A
Sequence 84331, A
Sequence 84331, A
Sequence 1056, Ap
Sequence 1056, Ap
Sequence 516, Appl
Sequence 516, Appl
Sequence 31978, A
   Sequence 690, Ap
Sequence 566557,
Sequence 291203,
Sequence 202708,
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
38.4	38.4	38.6	38.6	38.6	38.6	38.8	38.8	38.8	38.8	39	39.2	39.2	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.6	39.6	39.6	39.6
ω. 4.	3. <sub>4</sub>	۵. 4.	3.4	3.4	3.4	3.4	3.4	٠ <u>.</u>	3.4	<u>د</u> .	з. 5	3.5	з .5	3.5	3. <sub>5</sub>	ω .5	3.5	3.5	ω. 5	ω .5	3.5	3.5	3.5	3.5
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Sequence 239, App	Ξ.	Sequence 211, App	Sequence 905, App	Sequence 6, Appli	Sequence 843639,	Sequence 685537,	Sequence 77488, A	Sequence 77487, A	Sequence 172188,	Sequence 23149, A	Sequence 3, Appli	Sequence 163852,	Sequence 155, App	Sequence 4, Appli	Sequence 154, App	Sequence 7, Appli	Sequence 714153,	Sequence 774116,	Sequence 149500,	Sequence 149499,	Sequence 155, App	Sequence 4, Appli	Sequence 55400, A	Sequence 55400, A

## ALIGNMENTS

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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 605854
LENGTH: 627
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                        Match 3.8%;
Local Similarity 54.4%;
121 CGTTGCTACAAATAACACCGTCTTCTAGAGCTTCACCGT 160
                                                                                                                                                                                235
                                                                                                                                                                                                                                                                                     87; Conservative
                                                                                                                                                                                                                   AGAAATGATTGTCCAGGTCAAAAATTCAAAAGAAATTTTTTAAACTTCAAAAGTGAATGA
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PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR EFLING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEG ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
SEG ID NO 343968
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; Publication No. US/20060040262A1
; GENERAL INPOMATION:
   APPLICANT: David W. Morris
   APPLICANT: Marc Malandro
   TITLE OF INVENTION: Movel Compositions and Me
; TITLE REFERENCE: 529452001300
; CURRENT FAPPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
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US-09-925-065A-343968
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; LOCATION: (1):...(135462)
; OTHER INFORMATION: n = A,T,C or
US-10-330-773-37
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US-10-330-773-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Huma
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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ORGANISM: Mus musculus
FEATURE:
       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTTAAGCTTTTAGAATGGAAGCAATTGCTTGCATAGTTAGAATGTTGGTGT-GGAGCTC 124471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAAAAAAAAAGAAACAAAACAAAAAAAAAAAAACCAGGACCTGTGCTTTCCCAAGTTCTTA 124412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTATGTTTATCAATATCATAGGCTATAAGATCAGTATCCT 394
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Pred. No.
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                                                                                                             RESULT 5
US-10-947-249-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-09-925-065A-343967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
Sequence 91, Application US/10947249
Publication No. US20050287541A1
GENERAL INFORMATION:
APPLICANT: Akira NAKAGAWARA
APPLICANT: Miki OHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 343967, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 85; Conserv
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION UMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                    1090 СТІТАЛІСТСЯССТСТТІВСТТАСЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛ 1135
                                                                                                                                                                                                                                                                                                                                1030 CTATTGTCAATATCATCAGCTTTTGTTGCTTATGGTTTTTACAAACTTATATTGTACAACT 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1037 CAATATCATCAGCTTTTGTTGCTTATGGTTTTACAAACTTATATTTGTACAACTCTTTAAG 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                      970 GAAATTCAAGAGTTTGAGGTTATCATGTAAACATAAGTTTTTCTTTAGGGGCTGGTTTTT 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 ACTATTCTTCCTCTTTTGTATGAAAAGATCTAACTAAAATATATTATAAAAAAGCATTCTT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 AATAGTGAGATATAATCAAATTAAGAGATTCAATGAYCTCATTACCAATTCATTTATTTT
                                                                                                                                                                                                           214 CATTCTTCCAAATTCCTGTTAACATTAAAAAAAAAAAAGAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 CCAAATTCCTGTTAACATTAAAAAAAAAAGAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             977 AAGAGTTTGAGGTTATCATGTAAACATAAGTTTTTCTTTAGGGGCTGGTTTTTCTATTGT 1036
                                                                                                                                                                                                                                                                                                                                                                                           94 RAAGAAAAATAGTGAGATATAATCAAATTAAGAGATTCAATGACCTCATTACCAATTCAT
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; Pred. No. 10;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40.8; D
Pred. No. 17;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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US-11-122-329-76
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RESULT 7
US-11-096-568A-12837
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                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-122-329-76
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; ORGANISM: Homo sapiens
US-10-947-249-91
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CURRENT APPLICATION NUMBER: US/10/947,249

CURRENT FILING DATE: 2004-09-23

PRIOR APPLICATION NUMBER: US 60/505,614

PRIOR APPLICATION NUMBER: 2003-09-25

NUMBER OF SEQ ID NOS: 200

SOPTWARE: PATENTIN VETSION 3.1

SEQ ID NO 91
                                                                                                                                                                                                                                 Query Match 3.6%;
Best Local Similarity 58.8%;
Matches 70; Conservative
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Best Local :
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APPLICANT: Voelkel, Norbert
APPLICANT: Coldren, Chris
TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using
TITLE OF INVENTION: Expression Analysis of Peripheral Blood Cells
FILE REFERENCE: 2848-54
CURRENT APPLICATION NUMBER: US/11/122,329
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/568,129
PRIOR FILING DATE: 2004-05-03
NUMBER: OF SEQ ID NOS: 128
NUMBER: OF SEQ ID NOS: 128
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Geraci, Mark
APPLICANT: Bull, Todd
APPLICANT: Voelkel, Nor
APPLICANT: Coldren, Chr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yasuko YOSHIDA
APPLICANT: Saichi YAMADA
TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma and
TITLE OF INVENTION: Predicting the Prognosis of Neuroblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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Local Similarity 58.8%;
les 70; Conservative
                                                                                                      1017 GGGGCTGGTTTTTCTATTGTCAATATCATCAGCTTTTGGTTGCTTATGGTTTTACAAACTT 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1584 GGGGAAGGATTGGGTCTTGTCCCCCAACACACCTTCTGTGGCTGACTGTAATACTGTACA 1643
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                                                                                                                                                       1584 GGGGAAGGATTGGGTCTTGTCCCCCAACACAGCTTCTGTGGCTGACTGTAATACTGTACA 164:
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                                                                           Hiroyuki KUBO
Takahiro HIRATA
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                                                                                                                                                                                                                                 Score 40.6; DB
Pred. No. 27;
0; Mismatches
                                                                                                                                                                                                                                   0,
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Pred. No. 27;
0; Mismatches
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                                                                                                                                                                                                                                                                       DB 12;
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2000-05-09
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; ORGANISM: Triticum aestivum
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1).-(1842)
OTHER INFORMATION: Ceres Seq. ID no. 14303706
US-11-096-568A-12837
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US-09-925-065A-84331
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 12837
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                                                                                                                                               Matches
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 84331, Application US/09925065A Publication No. US20040181048A1
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                                                                                                                                                                         Query Match 3.5%;
Best Local Similarity 84.9%;
                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 652
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Local Similarity 65.6%;
                                     1046 CAGCTTTTGTTGCTTATGGTTTTACAAACTTTATATTGTACAACTCTTTTAAGTCACCTCTT
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TGTGTTTGAAAAAAAAAAAAAAAAAAAAAA 1791
                                                                                                                                               Conservative
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Pred. No. 30;
                                                                                                                                                                         Score 40.2;
Pred. No. 24;
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RESULT 9 US-09-925-065A-84332

Sequence 84332, Application US/09925065A Publication No. US20040181048A1

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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Uncleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 84332
LENGTH: 652
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-84332
                US-11-051-720-1711
Sequence 1711, Application US/11051720
Publication No. US20060046257A1
GENERAL INFORMATION:
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US-11-050-857-1056
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Publication No. US20060040278A1

GENERAL INFORMATION:

APPLICANT: Compugen Ltd

TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES,

TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 1847.105

CURRENT APPLICATION NUMBER: US/11/050,857

CURRENT FILING DATE: 2005-01-27
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Best Local :
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LENGTH: 2201
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APPLICANT: Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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Similarity 84.9%;
45; Conservative
                                                                                                                                                             AAAAAAAAAAAAAAAA 2198
                                                                                                                                                                                                AAAAAAAAAAAAAAAA 1135
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                                                                                                                                                                                                                                                                               TTATGGTTTTACAAACTTATATTGTACAACTCTTTAAGTCACCTCTTTGCTTACAAAAA 1118
                                                                                                                                                                                                                                                                                                                    3.5%;
ilarity 70.1%;
Conservative
                                                                                                                                                                                                                                                                                                                    Score 40.2; D
Pred. No. 35;
0; Mismatches
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Pred. No. 24;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-043-590-46
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                                                                                                                                                                                                                                                                                   RESULT 13
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CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 516
LENGTH: 2201
                                                                                                                                                                  Sequence 46, Application US/11043590
Publication No. US20050277156A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: Novel Brain Natriuretic
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                                                  NUMBER OF SEQ ID NOS: 47
SEQ ID NO 46
LENGTH: 2201
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                                                                                                             FILE REFERENCE: 1847.1011
CURRENT APPLICATION NUMBER: US/11/043,590
CURRENT FILING DATE: 2005-01-27
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TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences,
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
FILE REFERENCE: 1847.1003
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TYPE: DNA
ORGANISM: Homo Bapiens
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TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 35;
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Pred. No. 35;
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                                                                                                                                                                     Peptide Variants and Methods of
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RESULT 15
US-10-750-185-31978
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US-09-925-065A-325092
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US-09-925-065A-325092
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PRIOR FILLING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILLING DATE: 2000-11-20
PRIOR FILLING DATE: 2000-11-30
PRIOR FILLING DATE: 2000-11-30
PRIOR FILLING DATE: 2001-01-16
PRIOR FILLING DATE: 2001-01-16
                                                                                                                                                                                             Sequence 31978, Application US/10750185 Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 325092
                                                                                                                                                                             GENERAL INFORMATION:
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Best Local
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Best Local Similarity
                                                                                                                 APPLICANT: MMI GENOMICS, INC. APPLICANT: DeNISE, Sue K. APPLICANT: KERR, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/289,846 PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 108827.135
ICANT: BATES, Stephen ICANT: FANTIN, Dennis OF INVENTION: COMPOSITIONS REFERENCE: MMII100-2
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                                                                                                                                                                                                                                                                                                                                                                                                                           62 GAAACGCCTTTGAAGATGGCAAATACAAATCAAATCTCTTAACCTTGGACTCATCATCTC 121
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Similarity 55.1%;
76; Conservative
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                                                                              ROSENFELD, David
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llarity 70.1%;
Conservative
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; Pred. No. 35;
0; Mismatches
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                      FOR INFERRING
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                      BOVINE TRAITS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 31978
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 139; Conserv
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                       1044 ATCAGCTTTTGTTGCTTATGGTTTTACAAACTTATATTGTACAACTCTTTAAGTCACCTC 1103
                                  1104 TTTG 1107
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TTAG 845
                                                                     ACCAGATTCAGTTGCTTATGAGCTTGCCCATTCAGAAGTCTTTCCTCAATAGAAAAACCC
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Conservative
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1: /ggn2_6/ptodata/l/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/l/ina/5_COMB.seq:*

3: /ggn2_6/ptodata/l/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/l/ina/6A_COMB.seq:*

5: /ggn2_6/ptodata/l/ina/PTUS_COMB.seq:*

6: /cgn2_6/ptodata/l/ina/PTUS_COMB.seq:*

7: /ggn2_6/ptodata/l/ina/PE_COMB.seq:*

8: /cgn2_6/ptodata/l/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/l/ina/RE_COMB.seq:*
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US-09-247-373B-25

US-09-247-373B-25

US-09-247-373B-25

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US-09-296-13

US-09-033-2129-13

US-09-008-6978-11

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US-09-008-6978-11

US-09-018-568-1

US-09-917-254-31

US-09-917-254-31

US-09-917-254-36

US-09-015-051-36

US-09-005-051-36

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US-09-403-942F-38
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Sequence 16, Appl
Sequence 11283, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 36, Appl
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CURRENT FILING DATE: 1999-12-14
EARLIER FILING DATE: 1999-6-15
EARLIER FILING DATE: 1999-66-15
EARLIER FILING DATE: 1999-66-15
EARLIER APPLICATION NUMBER: 60/089,507
EARLIER APPLICATION NUMBER: 60/089,508
EARLIER APPLICATION NUMBER: 60/089,509
EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,510
EARLIER APPLICATION NUMBER: 60/090,112
EARLIER APPLICATION NUMBER: 60/090,112
EARLIER FILING DATE: 1998-06-22
EARLIER FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: 60/090,113
EARLIER FILING DATE: 1998-06-22
EARLIER FILING DATE: 1998-06-16
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APPLICANT: Ruben et al.

TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: PZ029P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                              1027 TTTCTATTGTCAATATCATCAGCTTTTGTTGCTTATGGTTTTACAAACTTATATTGTACA 1086
                                                                                                                      967 GTTGAAATTCAAGAGTTTTGAGGTTATCATGTAAACATAAGTTTTTTCTTTTAGGGGCTGGTT 1026
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Similarity 53.8%;
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6475753
        Conservative
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US-08-545-196B-12
US-08-545-196B-12
US-08-056-4
US-08-076-093A-3
US-08-076-093A-3
US-08-076-093A-3
US-08-08-076-093A-3
US-08-08-201-266-3
US-08-08-201-28-3
US-08-801-228-3
US-08-801-228-3
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US-08-801-228-3
US-08-801-228-3
US-08-91-104-28-3
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: PZ029G30AP1D2
CURRENT APPLICATION NUMBER: US/10/115,123
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: PCT/US99/13418
PRIOR APPLICATION NUMBER: PCT/US99/13418
PRIOR FILING DATE: 1999-06-15
PRIOR FILING DATE: 1998-06-16
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US-10-012-542-30
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Patent No. 677421
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Best Local
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PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-16
PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-16
PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-16
PRIOR PILING DATE: EARLIER APPLICATION NUMBER: 60/090,112
PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-22
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CURRENT APPLICATION NUMBER: US/10/012,542
CURRENT FILING DATE: 2001-12-12
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TITLE OF INVENTION: 94 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
LOCATION: (968)
OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                                                                                                                                                                                                                                                                 TTTCTATTGTCAATATCATCAGCTTTTGTTGCTTATGGTTTTACAAACTTATATTGTACA 1086
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PRIOR FILLING DATE: 1998-06-16
PRIOR FILLING DATE: 1998-06-22
PRIOR FILLING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090,113
PRIOR APPLICATION NUMBER: 60/090,113
PRIOR FILLING DATE: 1998-06-22
PRIOR FILLING DATE: 1998-06-22
PRIOR FILLING DATE: 1998-06-22
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                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (968)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1979
                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                            1802
1027 TTTCTATTGTCAATATCATCAGCTTTTGTTGCTTATGGTTTTACAAACTTATATTGTACA 1086
                                                                                                                                                                                967
                                                                                                                                                                                                                91;
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                                  GTTCAAAGTCTAGCTATTGGTATAATCATCTAATATTATATATCTCCAGTGCCCCTGA 1861
                                                                                                                                                                              GTTGAAATTCAAGAGTTTGAGGTTATCATGTAAACATAAGTTTTTCTTTAGGGGCTGGTT 1026
                                                                        Conservative
                                                                                                                                                                                                                                   3.9%;
                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                   Score 44.2; DB Pred. No. 0.084;
                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                    78;
                                                                                                                                                                                                                                                    Length 1979;
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US-08-330-108-16 RESULT 4 Sequence - ... Sp5752
Patent No. 5795752
GENERAL INFORMATION:
Smith, Kendall A.
ADPLICANT: Smith, Kendall A. Sequence 16, Application US/08330108 FILING DATE:
APPLICATION NUMBER: US/07/796,066
FILING DATE:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 base pairs COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,108 CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1 CORRESPONDENCE ADDRESS: TITLE OF INVENTION: IL-2-Stimu NUMBER OF SEQUENCES: COUNTRY: CITY: Boston STREET: FILING DATE: ADDRESSEE: 02109 Massachusetts: U.S.A. E: Lahive & Cockfield 60 State Street IL-2-Stimulated Gene US/08/104,736

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RESULT 5
PCT-US92-10087-16
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GENERAL INFORMATION:
APPLICANT: Smith, Kendall A.
TITLE OF INVENTION: IL-2-Stimulate
TITLE OF INVENTION: Expression
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                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/796,066
APPLICATION UNMBER: 1991
AFTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION UNMBER: 31,503
REFERENCE/DOCKET NUMBER: DCI-02
                                                                                                                                                                                   TELEFAX: 617-227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: c
HYPOTHETICAL: nc
                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 198 base pairs
TYPE: NUCLEIC ACID
           ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: human
CELL TYPE: T-cell blast
                                                                       HYPOTHETICAL:
                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19921118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
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ORGANISM: hum
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IMMEDIATE SOURCE
                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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CELL TYPE: T-cell blast
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Similarity 60.9%;
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Pred. No. 0.064;
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; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-11283
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                                                                                                                                                                       Sequence 25, Application US/08924747
Patent No. 6063570
GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF INVENTION: ENZYMES
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11283, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION UMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
NUMBER OF SEQ ID NOS: 62517
                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. DU PONT DE
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
                              COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
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CLONE: 8
COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MICROSOFT
                                                                   ZIP: 19898
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                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           997 TAAACATAAGTTTTTCTTTAGGGGCTGGTTTTTCTATTGTCAATATCATCAGCTTTTTGTT
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                                                                                   UNITED STATES OF AMERICA
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                                 DISKETTE, 3.50 INCH
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MICROSOFT WORD FOR WINDOWS
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Pred. No. 0.19;
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 95
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SEQUENCE CHARACTERISTICS:
LENGTH: 991 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                               ; SOFTWARE: Microsoft
SEQ ID NO 25
; LENGTH: 991
; TYPE: DNA
; ORGANISM: SOYBEAN
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/09247373B Patent No. 6168954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.7%;
Best Local Similarity 54.5%;
Matches 85; Conservative
                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6168954
GENERAL INFORMATION:
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ANTI-SENSE: NO
ORIGINAL SOURCE:
TISSUE TYPE: SOYBEAN
IMMEDIATE SOURCE:
CLONE: SSM.PK0067.G5
                                                                                                                                   -09-247-373B-25
                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/247,373B CURRENT FILING DATE: 1999-02-10
                                                                                                                                                                                                                                                                                                                                 APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF TRANSFERASE ENZYMES
TO THE TRANSFERASE ENZYMES
                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL
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                             980 AGTTTGAGGTTATCATGTAAACATAAGTTTTTCTTTAGGGGCTGGTTTTTCTATTGTCAA 1039
                                                                                                                                                                                                                      Microsoft Office 97
AGTATGATTTTGTTGGGAAACAATTATCTTGTTGTGAGCAAAGGATTGTTCTGTTTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           САСТТТАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА
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                                                                               3.7%;
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                                                                               Score 42.4; DB 3; Length 991; Pred. No. 0.19;
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Pred. No. 0.19;
0; Mismatches 71;
                                                                Mismatches
                                                             71;
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
TISSUE TYPE: SOYBEAN
IMMEDIATE SOURCE:
CLONE: SEM.PK0067.G5
US-09-296-715-25
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                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                           Query Match 3.7%;
Best Local Similarity 54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25, Application US/09296715 Patent No. 6171839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: PLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1
TELECHONEUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEPAX: 302-773-0164
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APPLICANT: O'KEEFE, D
TITLE OF INVENTION: S
TITLE OF INVENTION: I
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CORRESPONDENCE ADDRESS: 1. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS
SOFTWARE: MICROSOFT WORD VERSION 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                             1100 CCTCTTTGCTTACAAAAAAAAAAAAAAAAAAAA 1135
                                                                                                      1040 TATCATCAGCTTTTGTTGCTTATGGTTTTACAAACTTATATTGTACAACTCTTTAAGTCA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1040 TATCATCAGCTTTTGCTTATGGTTTTACAAACTTATATTGTACAACTCTTTAAGTCA 1099
                                                                                                                                       800 AGTATGATTTTGTTGGGAAACAATTATCTTGTTGAGCAAAGGATTGTTCTGTTTTAAA
                                                                                                                                                                        980 AGTTTGAGGTTATCATGTAAACATAAGTTTTTCTTTAGGGGGCTGGTTTTTCTATTGTCAA 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 920 САСТТТАЛЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛ
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                                                                                                                                                                                                          85;
CCTCTTTGCTTACAAAAAAAAAAAAAAAAAAAAAAA 1135
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                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CL-1108
                                                                                                                                                                                                                           Score 42.4; DB 3; Pred. No. 0.19;
                                                                                                                                                                                                          71;
                                                                                                                                                                                                                                             Length 991;
                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                          Gaps
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RESULT 10 US-09-832-129-13

Patent No. 69366

Application US/09832129

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                                                                                                                                         ; TYPE: DNA; ORGANISM: Buchnera US-09-790-988-1
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; ORGANISM: Homo mapiens
US-09-832-129-13
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US-09-790-988-1/c
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APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Fiscella et al.
TITLE OF INVENTION: 19 Human secreted proteins
FILE REFERENCE: PZ045P1
CURRENT APPLICATION NUMBER: US/09/832,129
CURRENT FILING DATE: 2001-04-11
                                                                       Matches
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09790988 Patent No. 6632935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTMARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US00/28664
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/163,085
PRIOR FILING DATE: 1999-11-02
PRIOR APPLICATION NUMBER: 60/172,411
PRIOR FILING DATE: 1999-12-17
                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 081356/0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 70
                                                                                                                                                                                             LENGTH: 640681
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                                                                                        Local
3251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1134 AA 1135
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                      968 TTGAAATTCAAGAGTTTGAGGTTATCATGTAAACATAAGTTTTTCTTTAGGGGCTGGTTT 1027
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                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA 3252
                                                                   3.7%;
ilarity 57.8%;
Conservative
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(larity 59.0%;
Conservative
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                                                                  Score 41.6; DB Pred. No. 5.5; 0; Mismatches
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                                                                                                    DB 3;
                                                                     54;
                                                                                                    Length 640681;
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CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/095,325
PRIOR FILING DATE: 1998-08-04
PRIOR PELICATION NUMBER: 60/112,851
PRIOR PELICATION NUMBER: 60/113,145
PRIOR PELICATION NUMBER: 60/113,145
PRIOR PELICATION NUMBER: 60/113,145
PRIOR APPLICATION NUMBER: 60/113,511
PRIOR FILING DATE: 1998-12-16
PRIOR PELICATION NUMBER: 60/115,558
PRIOR PELICATION NUMBER: 60/115,558
PRIOR PELICATION NUMBER: 60/115,558
PRIOR PELICATION NUMBER: 60/115,565
PRIOR PELICATION NUMBER: 60/115,733
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APPLICANT:
APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2930R1C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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OR APPLICATION NUMBER: PCT/US99/28634
OR FILING DATE: 1999-12-01
OR PPLICATION NUMBER: PCT/US99/28551
OR FILING DATE: 1999-12-02
OR APPLICATION NUMBER: PCT/US00/03565
OR FILING DATE: 2000-02-11
OR APPLICATION NUMBER: PCT/US00/04414
OR FILING DATE: 2000-02-22
OR APPLICATION NUMBER: PCT/US00/05841
OR APPLICATION NUMBER: PCT/US00/05843
OR APPLICATION NUMBER: PCT/US00/08439
OR FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                   OR APPLICATION NUMBER: 60/119,341
OR FILING DATE: 1999-02-09
OR FILING DATE: 1999-02-10
OR APPLICATION NUMBER: 60/119,537
OR FILING DATE: 1999-02-10
OR APPLICATION NUMBER: 60/119,965
OR APPLICATION NUMBER: 60/162,506
OR FILING DATE: 1999-10-29
OR APPLICATION NUMBER: 60/170,262
OR APPLICATION NUMBER: 60/187,202
OR FILING DATE: 1999-12-09
OR APPLICATION NUMBER: 60/187,202
OR FILING DATE: 1999-12-09
OR FILING DATE: 1909-12-09
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US99/12252
FILING DATE: 1999-06-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gurney, Austin L.
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; ORGANISM: Homo sapiens
US-10-033-301-23
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                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,697A
FILING DATE: January 19, 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chan, Albert Wal-Kit
REGISTRATION NUMBER: 36,479
REFERENCE/DOCKET NUMBER: 50752-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application Patent No. 6197504
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 38
SEQ ID NO 23
Matches
                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2186
                                                                               TOPOLOGY: li
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chow, Kir
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
Local Similarity
nes 67; Conserv
                                                                                                               LENGTH: 1278 base pairs TYPE: nucleic acid STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1185 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             982 TTTGAGGTTATCATGTAAACATAAGTTTTTCTTTAGGGGCTGGTTTTTCTATTGTCAATA 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACATTTGATTTTTTCACGTAAGTCCACATATACTTCTATAAGAGCGTGACTTGTAATAAA 2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
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NVENTION: USES OF MAB-21
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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              3.5%;
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0
              Score 40; DB 3
Pred. No. 0.97;
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Mismatches
                              DB 3; Length 1278;
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45; Indels
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US-08-148-209A-1
                                                                                                                                     Matches
                                                                                                                                                                   Query Match
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Patent No. 5556780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,209A
FILING DATE: 05-NOV-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 398-324
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2862 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dzau, Vict
APPLICANT: Mukoyama,
                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                  Local Similarity
es 64; Conserv
                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
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 2807
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                               1032 ATTGTCAATATCATCAGCTTTTGTTTGCTTATGGTTTTACAAACTTATATTGTACAACTCT 1091
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                                                                                                                                                                                                                                                                                                                   nucleic acid
ТАЛАЛТАЛАЛ TCATTACTGGGALAALAALAALAALAALAALAALAALAA 2850
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                                                                   ATAGCTAAATATGTAATCAGTTATGACTTTGTGTTTTAAGCAATTTTACACAAAATCTCG 2806
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                                                                                                                                                                                                                                                                                                                                  2862 base pairs
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                                                                                                                                   Conservative
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132..1223
                                                                                                                                                                                                                                                                                     linear
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05-NOV-1993
                                                                                                                                                                                                                                                                                                       double
                                                                                                                                                61.5%;
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                                                                                                                                  Score 40; DB 2
Pred. No. 1.4;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version
                                                                                                                                                                   DB 2;
                                                                                                                                   40;
                                                                                                                                                                 Length 2862;
                                                                                                                                   Indels
                                                                                                                                  0; Gaps
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RESULT 15 US-09-881-556A-1

Sequence 1, Application US/09881556A Patent No. 6808900 GENERAL INFORMATION:

APPLICANT: Simonsen,

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Page 7
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გ ई TITLE OF INVENTION: Cryptosporidium Parvum Antigens, Antibodies Thereto and Diagnosti
TITLE OF INVENTION: Therapeutic Compositions Thereof
FILE REFERRENCE: SASK-008/01US/09/881,556A
CURRENT APPLICATION NUMBER: US/09/881,556A
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/212,083
PRIOR FILING DATE: 2000-06-15
NUMBER: 0F SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
SEQ ID NO 1
CRGANISM: Cryptosporidium parvum
US-09-881-556A-1 밁 밁 Search completed: March 20, 2006, 14:05:56 Job time: 229.218 secs 밁 ঠ Query Match 3.5%; Score 39.6; DB 3; Length 1380; Best Local Similarity 57.1%; Pred. No. 1.3; Matches 72; Conservative 0; Mismatches 54; Indels 0 1359 AAAAAA 1364 1010 TTCTTTAGGGGCTGGTTTTTCTATTGTCAATATCATCAGCTTTTGTTGCTTATGGTTTTA 1069 1130 AAAAAA 1135 0; Gaps But he TEARS! MAIL

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